

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 05:56:54 ; Search time 3238.46 Seconds
(without alignments)
4666.271 Million cell updates/sec

Title: US-10-081-969-93
Perfect score: 397
Sequence: 1 cctcgtggtccctgca.....tggcccccggccaccccccgcg 397

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	95.4	24.0	1675	9 AG360980	Mus muscu
C 2	90.8	22.9	935	9 CNS006XK	AL066051 Drosophil
C 3	90.8	22.9	1146	5 BU955946	AGENCOURT
C 4	90.4	22.8	1020	6 CA792179	AGENCOURT
C 5	87.6	22.1	967	5 BQ678596	AGENCOURT
C 6	87.6	22.1	995	5 BQ939901	AGENCOURT
C 7	87.2	22.0	944	5 BU516035	AGENCOURT
C 8	87	21.9	807	7 CF149720	AGENCOURT
C 9	87	21.9	963	5 BU503665	AGENCOURT
C 10	87	21.9	972	5 BQ900341	AGENCOURT
C 11	86.4	21.8	925	9 CNS0081P	AL053013 Drosophil
C 12	86.2	21.7	982	9 CL473807	SAIL 207
C 13	86.2	21.7	1203	9 CNS015Y4	AL106054 Drosophil
C 14	85.8	21.6	1162	5 BQ051092	AGENCOURT
C 15	85.6	21.6	1088	5 BU505362	AGENCOURT
C 16	85.4	21.5	1048	5 BU529717	AGENCOURT
C 17	85.2	21.5	671	8 BH997981	BH997981 oeg69a02.
C 18	84.8	21.4	1136	5 BQ943816	AGENCOURT
C 19	84.6	21.3	943	4 BM415351	OP20425 M
C 20	84.4	21.3	1135	9 AG383043	Mus muscu
C 21	84.2	21.2	776	9 CNS010RY	AL099352 Drosophil
C 22	84.2	21.2	926	9 CL497807	SAIL 647
C 23	84.2	21.2	1021	5 BQ434910	AGENCOURT
C 24	84.2	21.2	1057	5 BU526464	AGENCOURT

C 25	83.8	21.1	932	9 CNS0072Q	AL066742 Drosophil
C 26	83.6	21.1	986	9 CL473390	SAIL 199
C 27	83.6	21.1	1080	8 AQ893056	HS 4832 A
C 28	83.6	21.1	1462	9 AG411877	Mus muscu
C 29	83.4	21.0	918	4 BG809598	mgct001xb
C 30	83.4	21.0	1141	9 CL082639	CH216-168
C 31	83.4	21.0	1273	4 BM562099	AGENCOURT
C 32	83.4	21.0	1474	8 BZ569821	msmh2_1034
C 33	83.2	21.0	825	9 AG081347	Pan trogl
C 34	83.2	21.0	1169	4 BM549879	AGENCOURT
C 35	82.8	20.9	1190	5 BQ673485	AGENCOURT
C 36	82.8	20.9	1692	9 AG396765	Mus muscu
C 37	82.6	20.8	942	5 BQ681469	AGENCOURT
C 38	82.6	20.8	974	9 AG071677	Pan trogl
C 39	82.6	20.8	985	5 BQ672571	AGENCOURT
C 40	82.6	20.8	1048	5 BU146089	AGENCOURT
C 41	82.4	20.8	1523	9 AG448267	Mus muscu
C 42	82.4	20.8	1619	9 AG435648	Mus muscu
C 43	82.4	20.8	1822	9 AG435170	Mus muscu
C 44	82.2	20.7	966	9 CL462945	SAIL 1173
C 45	82.2	20.7	1830	9 CL078620	CH216-151

ALIGNMENTS

RESULT 1
AG360980/c 1675 bp DNA linear GSS 03-JUN-2004
LOCUS Mus musculus molossinus DNA, clone:MSMG01-161J23.T7, genomic survey
DEFINITION sequence.
ACCESSION AG360980
VERSION AG360980.1 GI:47972185
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
REFERENCE 2 (bases 1 to 1675)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
TITLE Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22, Shuhiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@sc.riken.jp, URL:http://hgp.gsc.riken.go.jp/;
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@tc.riken.jp).
Taikuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@tc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY : pBACe3.6
R.Site 1 : EcoRI.
R.Site 2 : EcoRI.
FEATURES
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/db_xref="taxon:57486"
/clone="MSMG01-161J23.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMG01 Mouse Male BAC Library"

ORGANIZACIJA METANOGENOSTI

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/rao_nucleo_burub (pMGC 1001846)
/clone_lib="NIH MGC 107"
/notes-organ_breast_Vector: pOTB7; Site 1: EcoRI;

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13


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Plate: LLAMI3877 row: f column: 23
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6390550"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_129"
/note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;
Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Average insert size 2.2 kb. Constructed
by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
Library."

FEATURES
source
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Db 917 GCCGGCCGGGNGGNGGCGCCCGCGGGGGCGCGCGCGCGGCGGCGG 858
Qy 78 CCCGAGCAGCTGCGCTGTTCGCGGCGAGCGCGGCTCCAGTGGATTTCGCGGGCAGAC 137
Db 857 CGGCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 798
Qy 138 GCCCAGGACCGCGCTTCCACGTCGGGAGGAGTGGGGACCGCGGACCGTCTGCGCC 197
Db 797 GGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 738
Qy 198 CTTACACTTCGAGCTCCGCTTCTCCGCGCGAGACCGCGCGCGCGCGCGCGCGCG 257
Db 737 NNCNCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 678
Qy 258 TCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 317
Db 677 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 618
Qy 318 CCTCTCTCGCGCGCGCGAGTTTCAGGCGCGCTGCTGTCGCGCAGCTGGGAGCGCC 377
Db 617 CCCCCCNCCNCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 558
Qy 378 TGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 394
Db 557 CNGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 541

RESULT 7
BU516035/c
LOCUS
DEFINITION
AGENCOURT 10137554 NIH_MGC_134 Mus musculus cDNA clone
IMAGE:6512731 5', mRNA sequence.
ACCESSION
BU516035
VERSION
BU516035.1 GI:22823561
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 944)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. David Rowe
cDNA Library Preparation: Invitrogen Corp
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
cDNA Library Arrayed by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

/clone="IMAGE:6263404"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

Query Match 22.1%; Score 87.6; DB 5; Length 967;
Best Local Similarity 49.2%; Pred. No. 2.1e-06;
Matches 183; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

Qy 25 GGGAGCGCGAGCGCGCGCGCGGGAAGCGCGCGCCAGACCCCGGTCCGCGCGAG 84
Db 944 GGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 885
Qy 85 CAGCTGCGCTGTTCGCGCGCGCGCGGCTCCAGTGGATTTCGCGGCGACAGACGCCAGG 144
Db 884 GGGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 825
Qy 145 ACCGCGCTTCCACAGTGGGAGGAGTGGGAGCGCGGCGCGCGCGCGCGCGCG 204
Db 824 CCGCGNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 765
Qy 205 TTCCAGCTCGGCTTCTCCGCGCGAGACCGCGCGCGCGCGCGCGCGCGCGCG 264
Db 764 CCCCCCCCCCCCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 705
Qy 265 CCGAGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 324
Db 704 CCGNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 645
Qy 325 TCGCGCGCGAGTTTCAGGCGCGGCTGCTGTCGTCGCGCAGTGGGAGCGCTGCGCC 384
Db 644 CCCCCCCCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 585
Qy 385 GGCACACCGCGC 396
Db 584 CNNNCCNCCNCC 573

RESULT 6
BQ93901/c
LOCUS
DEFINITION
AGENCOURT 8818583 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6390550
5', mRNA sequence.
ACCESSION
BQ93901
VERSION
BQ93901.1 GI:22355379
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 995)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
```


Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14042 row: j column: 07
High quality sequence stop: 430.
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6491334"
/tissue_type="retina"
/lab_host="NIH MGC 94"
/clone_lib="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

FEATURES
source
1. .963
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6491334"
/tissue_type="retina"
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/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 21.9%; Score 87; DB 5; Length 963;
Best Local Similarity 47.7%; Pred. No. 2.6e-06;
Matches 189; Conservative 0; Mismatches 207; Indels 0; Gaps 0;
QY 1 CCTCTGCTGGTCTCTGACCTTGGAGCGGAGCGCGCGCGGGGAGCGCGGC 60
DB 908 CCGCGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 849
QY 61 CCAGACCCCGGGTCCCGCGGAGCAGTGCCTCTCGGGGCGAGCGGGCTCCAGTG 120
DB 848 GCNCGCCCG 789
QY 121 GATTTCGGGGCACAGACGCCCGCGCGCTTCCACAGTGGCGAGGAGCTGGGGACCC 180
DB 788 GGGCGCGNGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 729
QY 181 GGGCAGCCCTCTGCGCCCTTACCTTCAGCTCGGCTCTCTCGGCGGAGACCGCGCGCG 240
DB 728 CCCCCCG 669
QY 241 TCCGACACCTCTCGGGTCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 668 NNCGGCG 609
QY 301 CTTTTCGGCG 360
DB 608 CCG 549
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DB 548 CCG 513

RESULT 10
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LOCUS
DEFINITION
AGENCY: 8750450 NIH_MGC_130 Mus musculus cDNA clone IMAGE:633156
5', mRNA sequence.
ACCESSION
BQ900341
VERSION
BQ900341.1 GI:22929355
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 972)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/.

EMAIL: cgapbs-r@mail.nih.gov
TISSUE PROCUREMENT: THE CEPKO LABORATORY
CDNA LIBRARY PREPARATION: LIFE TECHNOLOGIES, INC.
CDNA LIBRARY ARRAYED BY: THE I.M.A.G.E. CONSORTIUM (LLNL)
DNA SEQUENCING BY: AGENCOURT BIOSCIENCE CORPORATION
CLONE DISTRIBUTION: MGC CLONE DISTRIBUTION INFORMATION CAN BE FOUND THROUGH THE I.M.A.G.E. CONSORTIUM/LLNL AT:
HTTP://IMAGE.LLNL.GOV
PLATE: LLAM14042 ROW: J COLUMN: 07
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/DB_XREF="taxon:10090"
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/TISSUE_TYPE="retina"
/LAB_HOST="NIH MGC 94"
/CLONE_LIB="DH10B (phage-resistant)"
/NOTE="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

FEATURES
source
1. .963
/ORGANISM="Mus musculus"
/MOL_TYPE="mRNA"
/DB_XREF="taxon:10090"
/CLONE="IMAGE:6491334"
/TISSUE_TYPE="retina"
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/CLONE_LIB="DH10B (phage-resistant)"
/NOTE="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 21.9%; Score 87; DB 5; Length 963;
Best Local Similarity 47.7%; Pred. No. 2.6e-06;
Matches 189; Conservative 0; Mismatches 207; Indels 0; Gaps 0;
QY 1 CCTCTGCTGGTCTCTGACCTTGGAGCGGAGCGCGCGCGGGGAGCGCGGC 60
DB 908 CCGCGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 849
QY 61 CCAGACCCCGGGTCCCGCGGAGCAGTGCCTCTCGGGGCGAGCGGGCTCCAGTG 120
DB 848 GCNCGCCCG 789
QY 121 GATTTCGGGGCACAGACGCCCGCGCGCTTCCACAGTGGCGAGGAGCTGGGGACCC 180
DB 788 GGGCGCGNGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 729
QY 181 GGGCAGCCCTCTGCGCCCTTACCTTCAGCTCGGCTCTCTCGGCGGAGACCGCGCGCG 240
DB 728 CCCCCCG 669
QY 241 TCCGACACCTCTCGGGTCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 668 NNCGGCG 609
QY 301 CTTTTCGGCG 360
DB 608 CCG 549
QY 361 GGGCAGCTGGGAGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 396
DB 548 CCG 513

RESULT 11
CNS0091P
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly); genomic survey sequence.
ACCESSION
AL053013
VERSION
AL053013.1 GI:4934461
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman, Ph.D.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13791 row: o column: 13
High quality sequence stop: 413.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
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/clone="IMAGE:633156"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 130"
/note="Organ: oocyte; Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.95 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."

FEATURES
source
1. .972
/organism="Mus musculus"
/mol_type="mRNA"
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/clone="IMAGE:633156"
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/note="Organ: oocyte; Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.95 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 21.9%; Score 87; DB 5; Length 972;
Best Local Similarity 47.3%; Pred. No. 2.6e-06;
Matches 183; Conservative 0; Mismatches 204; Indels 0; Gaps 0;
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DB 769 GCG 710
QY 70 CGGGTCCCGCGGAGCAGCTGCGTGTGCGGGGCGAGCGCGGCTCCAGTTCGCGG 129
DB 709 CCCCCCG 650
QY 130 GCACAGAGCGCGAGACCGCGCTTCCACAGTGGCGGAGGAGTGGGAGACCGCG 189
DB 649 GCGGGGCG 590
QY 190 TCTGCGCGCTTACCTTCCAGCTCCGCTCTCTCGCGGGAGCGCGCGCGCGCG 249
DB 589 CCGNNCCCG 530
QY 250 CTCGGGCTCCCG 309
DB 529 CCG 470
QY 310 GCGCGCGCGCTCTCTCGCGGGGAGTTTACGAGCAGCGCTGCGTCTGCGCAGCG 369
DB 469 CCG 410
QY 370 GGAAGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 396
DB 409 NNGGCG 383

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1088)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM14047 row: m column: 06
High quality sequence stop: 116.

FEATURES

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6493325"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 21.6%; Score 85.6; DB 5; Length 1088;
Best Local Similarity 52.0%; Pred. No. 4.7e-06;
Matches 169; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
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Db |||||
499 CGCGCGGCG 440
QY 67 CCCCCGGTCCGCGGAGAGCTGCGTGTGGGGCCAGGCGGGCTCCAGTGGATTGG 126
Db |||||
439 CGCGGCG 380
QY 127 CGGGCAGAGCGCCAGGACCGCGTTCACGTGGCGGAGGACTGGGGACCGGGCAC 186
Db |||||
379 CCCCCCNCCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 320
QY 187 CCGTCTGCGCCCTTACCTTCAGCTTCGCGCTTCTTCGCGGGGACCCCGCGCCGTCCEGA 246
Db |||||
319 CCCCCCG 260
QY 247 CCGCTCCGCGGTCGCGGCGCGAGCGCGCTTCGCGGGGCTTCAGAGCGCTTCTTCTTC 306
Db |||||
259 CCCCCCG 200
QY 307 CGCGGCGCGCGCGCTCTCTCGCGGC 331
Db |||||
199 CCGNNCCCCCCCCCCCCCCCCCNC 175

Search completed: April 9, 2005, 10:27:42
Job time : 3246.46 secs

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 06:08:24 ; Search time 507.69 Seconds
(without alignments)
4738.760 Million cell updates/sec

Title: US-10-081-969-93

Perfect score: 397

Sequence: 1 cccctgtggcgtccctgca.....tggccccggcaccaccccgcg 397

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	397	100.0	397	15	US-10-081-969-93
2	397	100.0	4293	18	US-10-456-830-1
3	397	100.0	4321	17	US-10-325-810-6
4	397	100.0	15418	9	US-09-783-203-1
5	397	100.0	15418	9	US-09-994-427A-1
6	397	100.0	15418	10	US-09-995-419A-1
7	397	100.0	15418	14	US-10-141-220-1
8	397	100.0	15418	14	US-10-023-969-1
9	397	100.0	15418	14	US-10-206-447-1
10	397	100.0	15418	17	US-10-674-836-1
11	397	100.0	15418	18	US-10-811-012-1
12	397	100.0	15418	18	US-10-811-012-1
13	397	100.0	15418	18	US-10-811-012-1
14	397	100.0	15418	18	US-10-811-012-1
15	397	100.0	15418	18	US-10-811-012-1
16	397	100.0	15418	18	US-10-811-012-1
17	397	100.0	15418	18	US-10-811-012-1
18	397	100.0	15418	18	US-10-811-012-1
19	397	100.0	15418	18	US-10-811-012-1
20	397	100.0	15418	18	US-10-811-012-1
21	397	100.0	15418	18	US-10-811-012-1
22	397	100.0	15418	18	US-10-811-012-1
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25	397	100.0	15418	18	US-10-811-012-1
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33	397	100.0	15418	18	US-10-811-012-1
34	397	100.0	15418	18	US-10-811-012-1
35	397	100.0	15418	18	US-10-811-012-1
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38	397	100.0	15418	18	US-10-811-012-1
39	397	100.0	15418	18	US-10-811-012-1
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41	397	100.0	15418	18	US-10-811-012-1
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45	397	100.0	15418	18	US-10-811-012-1

12	395.4	99.6	5126	19	US-10-840-455-1	Sequence 1, Appli
13	395.4	99.6	11276	19	US-10-840-455-3	Sequence 3, Appli
14	395.4	99.6	26414	19	US-10-840-455-43	Sequence 41, Appli
15	395.4	99.6	51552	9	US-09-733-294A-30	Sequence 30, Appli
16	376.4	94.8	378	14	US-10-212-667-1	Sequence 1, Appli
17	354.2	89.2	35871	9	US-09-956-335-2	Sequence 2, Appli
18	354.2	89.2	35978	9	US-09-956-335-1	Sequence 1, Appli
19	351	88.4	1677	9	US-09-956-335-3	Sequence 3, Appli
20	341.8	86.1	4335	18	US-10-877-124-6	Sequence 6, Appli
21	341.8	86.1	4335	18	US-10-877-124-6	Sequence 6, Appli
22	341.8	86.1	4335	19	US-10-877-146-6	Sequence 6, Appli
23	338.8	85.3	4200	14	US-10-044-692-6	Sequence 6, Appli
24	338.8	85.3	4200	15	US-10-044-539-6	Sequence 6, Appli
25	310	78.1	460	18	US-10-456-830-6	Sequence 8, Appli
26	298.2	75.1	314	9	US-09-916-510A-8	Sequence 8, Appli
27	298.2	75.1	314	17	US-10-376-630-8	Sequence 8, Appli
28	297.2	74.9	361	18	US-10-456-830-8	Sequence 8, Appli
29	297.2	74.9	381	18	US-10-456-830-9	Sequence 9, Appli
30	295	74.3	298	17	US-10-674-836-17	Sequence 17, Appli
31	273.8	69.0	4356	17	US-10-240-589C-144	Sequence 144, App
32	260.4	65.6	327	19	US-10-483-289A-8	Sequence 8, Appli
33	259	65.2	293	19	US-10-483-289A-5	Sequence 5, Appli
34	256.4	64.6	261	10	US-09-932-581-24	Sequence 24, Appli
35	256.4	64.6	261	16	US-10-338-294-24	Sequence 24, Appli
36	256.4	64.6	261	19	US-10-863-075-24	Sequence 24, Appli
37	256.4	64.6	295	15	US-10-140-763A-12	Sequence 12, Appli
38	256.4	64.6	5928	10	US-09-932-581-25	Sequence 25, Appli
39	256.4	64.6	5928	16	US-10-338-294-25	Sequence 25, Appli
40	256.4	64.6	5928	19	US-10-863-075-25	Sequence 25, Appli
41	244	61.5	245	15	US-10-081-969-94	Sequence 94, Appli
42	244	61.5	955	15	US-10-081-969-17	Sequence 17, Appli
43	216.4	54.5	240	15	US-10-140-763A-13	Sequence 13, Appli
44	199.8	50.3	403	15	US-10-081-969-21	Sequence 21, Appli
45	181.2	45.6	4356	17	US-10-240-589C-143	Sequence 143, App

ALIGNMENTS

RESULT 1
US-10-081-969-93
; Sequence 93, Application US/10081969
; Publication No. US20030104625A1

- ; GENERAL INFORMATION:
- ; APPLICANT: Cheng, Cheng
- ; APPLICANT: Clarke, Lori
- ; APPLICANT: Connolly, Sheila
- ; APPLICANT: Ennist, David
- ; APPLICANT: Forry-Schaudies, Suzanne
- ; APPLICANT: Gorziglia, Mario
- ; APPLICANT: Hallenbeck, Paul
- ; APPLICANT: Hay, Carl
- ; APPLICANT: Jakubczak, John
- ; APPLICANT: Kaleko, Michael
- ; APPLICANT: Phipps, Sandrina
- ; APPLICANT: Police, Seshidhar
- ; APPLICANT: Ryan, Patricia
- ; APPLICANT: Steward, David
- ; APPLICANT: Xie, Yuefeng
- ; TITLE OF INVENTION: No. US20030104625A1el Oncolytic Adenoviral Vectors

FILE REFERENCE: 4-31704A/GTI
CURRENT APPLICATION NUMBER: US/10/081.969
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/270,922
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/295,037
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/348,670
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn version 3.1
SEQ ID NO 93
LENGTH: 397

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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(397)
; OTHER INFORMATION: A 397 bp fragment of the hTERT promoter
US-10-081-969-93

Query Match      100.0%; Score 397; DB 15; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.7e-82;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTGCTGGCTCCCTGACACCTTGGAGCGCGGCGCGCGGGGAAAGCGCGC 60
DB 1 CCTCTGCTGGCTCCCTGACACCTTGGAGCGCGGCGCGGGGAAAGCGCGC 60

QY 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTGGGGGCGAGCGGGTCCAGTG 120
DB 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTGGGGGCGAGCGGGTCCAGTG 120

QY 121 GATTCGCGGCGACAGACGCCCGGCTTCCACGCTGGCGGAGGACTGGGGACCC 180
DB 121 GATTCGCGGCGACAGACGCCCGGCTTCCACGCTGGCGGAGGACTGGGGACCC 180

QY 181 GGGACACCGTCTGCGCCCTTCACTTCCAGTCCGCTCTCCGCGCGAACCCCGCCG 240
DB 181 GGGACACCGTCTGCGCCCTTCACTTCCAGTCCGCTCTCCGCGCGAACCCCGCCG 240

QY 241 TCCGACCCCTCCCGGGTCCCGGCGAGCGCCCTCCGCGCCCTCCAGCCCTCCCTT 300
DB 241 TCCGACCCCTCCCGGGTCCCGGCGAGCGCCCTCCGCGCCCTCCAGCCCTCCCTT 300

QY 301 CTTTTCGCGGGCCCGCCCTCTCTCGCGCGCGAGTTTCAGGACGCTGGTCTCTGCT 360
DB 301 CTTTTCGCGGGCCCGCCCTCTCTCGCGCGCGAGTTTCAGGACGCTGGTCTCTGCT 360

QY 361 GCGCAGTGGGAAGCGCTGCGCCCGCGCACCCCGCG 397
DB 361 GCGCAGTGGGAAGCGCTGCGCCCGCGCACCCCGCG 397

RESULT 2
US-10-456-830-1
; Sequence 1, Application US/10456830
; Publication No. US20040248246A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; represented by the Secretary of the Department of Health and
; Human Services
; APPLICANT: Human Services
; APPLICANT: Horikawa, Izumi
; APPLICANT: Barrett, J. Carl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DIFFERENTIAL EXPRESSION
; FILE REFERENCE: 4239-63008
; CURRENT APPLICATION NUMBER: US/10/456,830
; CURRENT FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4293
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3545)..(3609)
; OTHER INFORMATION: Region identical to HBV integration site in huH-4 cell line
; FEATURE:
; NAME/KEY: protein bind
; LOCATION: (3729)..(3734)
; OTHER INFORMATION: Upstream E-box
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3915)..(3916)
; OTHER INFORMATION: Major transcription initiation site
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; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (3916)..(3970)
; OTHER INFORMATION: 5' untranslated region of mRNA
; FEATURE:
; NAME/KEY: protein bind
; LOCATION: (3937)..(3942)
; OTHER INFORMATION: Downstream E-box
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3971)..(4189)
; OTHER INFORMATION: Exon 1
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: (4029)..(4050)
; OTHER INFORMATION: GW2 primer binding site
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (4190)..(4293)
; OTHER INFORMATION: Intron 1
; US-10-456-830-1

Query Match      100.0%; Score 397; DB 18; Length 4293;
Best Local Similarity 100.0%; Pred. No. 8.5e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTCGTGGCTCCCTGACACCTTGGAGCGCGGCGCGGGGAAAGCGCGC 60
DB 3574 CCCTCGTGGCTCCCTGACACCTTGGAGCGCGGCGCGGGGAAAGCGCGC 3633

QY 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGGCTGTGGGGGCGAGCGGGGCTCCAGTG 120
DB 3634 CCAGACCCCGGGTCCCGCGGAGCAGCTGGCTGTGGGGGCGAGCGGGGCTCCAGTG 3693

QY 121 GATTCGCGGCGACAGACGCCCGGCTTCCACGCTGGCGGAGGACTGGGGACCC 180
DB 3694 GATTCGCGGCGACAGACGCCCGGCTTCCACGCTGGCGGAGGACTGGGGACCC 3753

QY 181 GGGACACCGTCTGCGCCCTTCACTTCCAGTCCGCTCTCCGCGCGAACCCCGCG 240
DB 3754 GGGACACCGTCTGCGCCCTTCACTTCCAGTCCGCTCTCCGCGCGAACCCCGCG 3813

QY 241 TCCGACCCCTCCCGGGTCCCGGCGAGCGCCCTCCGCGCCCTCCAGCCCTCCCTT 300
DB 3814 TCCGACCCCTCCCGGGTCCCGGCGAGCGCCCTCCGCGCCCTCCAGCCCTCCCTT 3873

QY 301 CTTTTCGCGGGCCCGCCCTCTCTCGCGCGCGAGTTTCAGGACGCTGGTCTCTGCT 360
DB 3874 CTTTTCGCGGGCCCGCCCTCTCTCGCGCGCGAGTTTCAGGACGCTGGTCTCTGCT 3933

QY 361 GCGCAGTGGGAAGCGCTGCGCCCGCGCACCCCGCG 397
DB 3934 GCGCAGTGGGAAGCGCTGCGCCCGCGCACCCCGCG 3970

RESULT 3
US-10-325-810-6
; Sequence 6, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```

STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Ausehus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 4321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: -
LOCATION: 1..4321
OTHER INFORMATION: /note= "genomic DNA insert of pGRN14"

FEATURE:

NAME/KEY: intron
LOCATION: 2702..2804
OTHER INFORMATION: /note= "intron 1"

FEATURE:

NAME/KEY: intron
LOCATION: 4160..4313
OTHER INFORMATION: /note= "intron 2"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-325-810-6

Query Match 100.0%; Score 397; DB 17; Length 4321;
Best Local Similarity 100.0%; Pred. No. 8.5e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTCGCTGGGTCCCTGCACCTCGGAGCGGAGCGCGCGCGCGGGAAGCGCGC 60
Db 2086 CCCTCGCTGGGTCCCTGCACCTCGGAGCGGAGCGCGCGCGGGAAGCGCGC 2145

Qy 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTCTCGGGGCGCAGCGCGGCTCCCATG 120

Db 2146 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTCTCGGGGCGCAGCGCGGCTCCCATG 2205

Qy 121 GATTGCGGGGCACAGACGCCAGACCGCGCTTCCACGTGCGCGAGGAGACTGGGGACCC 180
Db 2206 GATTGCGGGGCACAGACGCCAGACCGCGCTTCCACGTGCGCGAGGAGACTGGGGACCC 2265
Qy 181 GGGACACCGTCTGCGGCTTCCACCTTCCAGTCTCGGCTTCTCCGCGGAGACCGCGCGG 240
Db 2266 GGGACACCGTCTGCGGCTTCCACCTTCCAGTCTCGGCTTCTCCGCGGAGACCGCGCGG 2325
Qy 241 TCCGACCCCTCCCGGTCCCGGCGCCAGACCCCTTCCGCGGCTTCCAGACCCCTCCCTTT 300
Db 2326 TCCGACCCCTCCCGGTCCCGGCGCCAGACCCCTTCCGCGGCTTCCAGACCCCTCCCTTT 2385
Qy 301 CTTTTCGCGCGCGCGCTTCTTCTGCGCGCGGAGTTTTCAGGAGCGCTGCGTCTGCT 360
Db 2386 CTTTTCGCGCGCGCGCTTCTTCTGCGCGCGGAGTTTTCAGGAGCGCTGCGTCTGCT 2445
Qy 361 GCGACAGTGGGAAGCCCTGGGCGCGCCACCCCGCG 397
Db 2446 GCGACAGTGGGAAGCCCTGGGCGCGCCACCCCGCG 2482

RESULT 4

US-09-783-203-1
; Sequence 1, Application US/09783203
; Patent No. US20020098582A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tpacked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/09/783,203
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-783-203-1

Query Match 100.0%; Score 397; DB 9; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTCGCTGGGTCCCTGCACCTCGGAGCGGAGCGCGCGCGGGAAGCGCGC 60
Db 13148 CCCTCGCTGGGTCCCTGCACCTCGGAGCGGAGCGCGCGCGGGAAGCGCGC 13207

Qy 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTCTGCGGCGCGAGCGCGGCTCCCATG 120
Db 13208 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTCTGCGGCGCGAGCGCGGCTCCCATG 13267

Qy 121 GATTGCGGGGCACAGACGCCAGACCGCGCTTCCACGTGCGGAGGAGACTGGGGACCC 180
Db 13268 GATTGCGGGGCACAGACGCCAGACCGCGCTTCCACGTGCGGAGGAGACTGGGGACCC 13327

Qy 181 GGGACACCGTCTGCGGCTTCCACCTTCCAGTCTCGGCTTCCGCGGCGGAGACCGCGCGG 240
Db 13328 GGGACACCGTCTGCGGCTTCCACCTTCCAGTCTCGGCTTCCGCGGCGGAGACCGCGCGG 13387

Qy 241 TCCGACCCCTCCCGGTCCCGGCGCCAGACCCCTTCCGCGGCTTCCAGACCCCTCCCTTT 300
Db 13388 TCCGACCCCTCCCGGTCCCGGCGCCAGACCCCTTCCGCGGCTTCCAGACCCCTCCCTTT 13447

Qy 301 CTTTTCGCGCGCGCGCTTCTTCTGCGGCGCGAGTTTTCAGGAGCGCTGCGTCTGCT 360
Db 13448 CTTTTCGCGCGCGCGCTTCTTCTGCGGCGCGAGTTTTCAGGAGCGCTGCGTCTGCT 13507

Qy 1 CCCTCGCTGGCGTCCCTGCACCCCTGGAGCGGAGCGCGCGCGGGCGGGGAGCGCGGC 60
Db 13148 CCCTCGCTGGCGTCCCTGCACCCCTGGAGCGGAGCGCGCGCGGGCGGGGAGCGCGGC 13207
Qy 61 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGTGTGCGGGCCAGCGCGGCTCCCACTG 120
Db 13208 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGTGTGCGGGCCAGCGCGGCTCCCACTG 13267
Qy 121 GATTGCGGGGCACAGACCCCGAGCACCGCTTCCACGTGCGGAGGAGCTGGGGAGCC 180
Db 13268 GATTGCGGGGCACAGACCCCGAGCACCGCTTCCACGTGCGGAGGAGCTGGGGAGCC 13327
Qy 181 GGGCACCCGCTCCGCGCTTCCCTTCCAGCTCCGCTCCCTCCGCGGAGCCCGCGCGC 240
Db 13328 GGGCACCCGCTCCGCGCTTCCCTTCCAGCTCCGCTCCCTCCGCGGAGCCCGCGCGC 13387
Qy 241 TCCGACCCCTCCGCGTCCCGGCGCCAGCCCTCCGCGGCTCCAGCCCTCCCTT 300
Db 13388 TCCGACCCCTCCGCGTCCCGGCGCCAGCCCTCCGCGGCTCCAGCCCTCCCTT 13447
Qy 301 CCTTCCGCGCGCGCGCTTCTCTCGCGCGCGAGTTTCAGGACGCGCTCGTCTGCT 360
Db 13448 CCTTCCGCGCGCGCGCTTCTCTCGCGCGCGAGTTTCAGGACGCGCTCGTCTGCT 13507
Qy 361 GCGCAGTGGGAGCCCTGGCGCGCGCGCCACCCCGCG 397
Db 13508 GCGCAGTGGGAGCCCTGGCGCGCGCGCCACCCCGCG 13544

RESULT 8
US-10-023-969-1
; Sequence 1, Application US/10023969
; Publication No. US20030095989A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Irving, John
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Chimeric Cytolytic Viruses for Cancer Treatment
; FILE OF INVENTION: 084,002
; CURRENT APPLICATION NUMBER: US/10/023,969
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/256,418
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-969-1

Query Match 100.0%; Score 397; DB 14; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTCGCTGGCGTCCCTGCACCCCTGGAGCGGAGCGCGCGGGCGGGGAGCGCGGC 60
Db 13148 CCCTCGCTGGCGTCCCTGCACCCCTGGAGCGGAGCGCGCGGGCGGGGAGCGCGGC 13207
Qy 61 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGTGTGCGGGCCAGCGCGGCTCCCACTG 120
Db 13208 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGTGTGCGGGCCAGCGCGGCTCCCACTG 13267
Qy 121 GATTGCGGGGCACAGACCCCGAGCACCGCTTCCACGTGCGGAGGAGCTGGGGAGCC 180
Db 13268 GATTGCGGGGCACAGACCCCGAGCACCGCTTCCACGTGCGGAGGAGCTGGGGAGCC 13327
Qy 181 GGGCACCCGCTCCGCGCTTCCCTTCCAGCTCCGCTCCCTCCGCGGAGCCCGCGCGC 240
Db 13328 GGGCACCCGCTCCGCGCTTCCCTTCCAGCTCCGCTCCCTCCGCGGAGCCCGCGCGC 13387
Qy 241 TCCGACCCCTCCGCGTCCCGGCGCCAGCCCTCCGCGGCTCCAGCCCTCCCTT 300
Db 13388 TCCGACCCCTCCGCGTCCCGGCGCCAGCCCTCCGCGGCTCCAGCCCTCCCTT 13447
Qy 301 CCTTCCGCGCGCGCGCTTCTCTCGCGCGCGAGTTTCAGGACGCGCTCGTCTGCT 360
Db 13448 CCTTCCGCGCGCGCGCTTCTCTCGCGCGCGAGTTTCAGGACGCGCTCGTCTGCT 13507
Qy 361 GCGCAGTGGGAGCCCTGGCGCGCGCGCCACCCCGCG 397
Db 13508 GCGCAGTGGGAGCCCTGGCGCGCGCGCCACCCCGCG 13544

Db 13388 TCCGACCCCTCCGCGTCCCGGGTCCCGGGCCAGCCCTCCGCGGCTCCAGCCCTCCCTT 13447
Qy 301 CCTTCCGCGCGCGCGCTTCTCTCGCGCGCGAGTTTCAGGACGCGCTCGTCTGCT 360
Db 13448 CCTTCCGCGCGCGCGCTTCTCTCGCGCGCGAGTTTCAGGACGCGCTCGTCTGCT 13507
Qy 361 GCGCAGTGGGAGCCCTGGCGCGCGCGCCACCCCGCG 397
Db 13508 GCGCAGTGGGAGCCCTGGCGCGCGCGCCACCCCGCG 13544

RESULT 9
US-10-206-447-1
; Sequence 1, Application US/10206447
; Publication No. US20030099616A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Irving, John
; APPLICANT: Karpf, David
; APPLICANT: Schiff, Michael
; TITLE OF INVENTION: DUAL SPECIFICITY TUMOR KILLING VECTORS DRIVEN BY THE TELOMERASE P
; FILE OF INVENTION: 085/002
; CURRENT APPLICATION NUMBER: US/10/206,447
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,029
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-206-447-1

Query Match 100.0%; Score 397; DB 14; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTCGCTGGCGTCCCTGCACCCCTGGAGCGGAGCGCGCGGGCGGGGAGCGCGGC 60
Db 13148 CCCTCGCTGGCGTCCCTGCACCCCTGGAGCGGAGCGCGCGGGCGGGGAGCGCGGC 13207
Qy 61 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGTGTGCGGGCCAGCGCGGCTCCCACTG 120
Db 13208 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGTGTGCGGGCCAGCGCGGCTCCCACTG 13267
Qy 121 GATTGCGGGGCACAGACCCCGAGCACCGCTTCCACGTGCGGAGGAGCTGGGGAGCC 180
Db 13268 GATTGCGGGGCACAGACCCCGAGCACCGCTTCCACGTGCGGAGGAGCTGGGGAGCC 13327
Qy 181 GGGCACCCGCTCCGCGCTTCCCTTCCAGCTCCGCTCCCTCCGCGGAGCCCGCGCGC 240
Db 13328 GGGCACCCGCTCCGCGCTTCCCTTCCAGCTCCGCTCCCTCCGCGGAGCCCGCGCGC 13387
Qy 241 TCCGACCCCTCCGCGTCCCGGCGCCAGCCCTCCGCGGCTCCAGCCCTCCCTT 300
Db 13388 TCCGACCCCTCCGCGTCCCGGCGCCAGCCCTCCGCGGCTCCAGCCCTCCCTT 13447
Qy 301 CCTTCCGCGCGCGCGCTTCTCTCGCGCGCGAGTTTCAGGACGCGCTCGTCTGCT 360
Db 13448 CCTTCCGCGCGCGCGCTTCTCTCGCGCGCGAGTTTCAGGACGCGCTCGTCTGCT 13507
Qy 361 GCGCAGTGGGAGCCCTGGCGCGCGCGCCACCCCGCG 397
Db 13508 GCGCAGTGGGAGCCCTGGCGCGCGCGCCACCCCGCG 13544

RESULT 10
US-10-674-836-1
; Sequence 1, Application US/10674836
; Publication No. US20040072787A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.

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; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; TITLE OF INVENTION: Regulatory Sequences and Methods of Using
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/10/674,836
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/244,438
; PRIOR FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-10-674-836-1

Query Match      100.0%; Score 397; DB 17; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CCTCGCTGGCTCCTGACCTGGAGCGGAGCGGCGCGCGCGGGGGAAGCGCGGC 60
Db      13148  CCTCGCTGGCTCCTGACCTGGAGCGGAGCGGCGCGCGCGGGGGAAGCGCGGC 13207

QY      61  CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTCCGGGGCCAGCGGGCTCCACAGT 120
Db      13208  CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTCCGGGGCCAGCGGGCTCCACAGT 13267

QY      121  GATTGCGGGGCACAGACGCCCGAGGACCGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 180
Db      13268  GATTGCGGGGCACAGACGCCCGAGGACCGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 13327

QY      181  GGGCACCCGCTCTGCGCCCTTACCTTCCAGTCCGCTCTCCGCGCGGACCCCGCCCG 240
Db      13328  GGGCACCCGCTCTGCGCCCTTACCTTCCAGTCCGCTCTCCGCGCGGACCCCGCCCG 13387

QY      241  TCCGACCCCTCCGGGTCCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db      13388  TCCGACCCCTCCGGGTCCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 13447

QY      301  CTTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Db      13448  CTTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 13507

QY      361  GGCACGTGGGAAGCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 397
Db      13508  GGCACGTGGGAAGCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 13544

RESULT 11
US-10-811-012-1
; Sequence 1, Application US/10811012
; Publication No. US20040152189A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: McWhir, Jim
; APPLICANT: Gold, Joseph D.
; APPLICANT: Schiffl, J. Michael
; TITLE OF INVENTION: Selective Antibody Targeting of Undifferentiated Stem Cells
; FILE REFERENCE: 096.006D- SeqList
; CURRENT APPLICATION NUMBER: US/10/811,012
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: 09/995,419
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
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; PRIOR APPLICATION NUMBER: 60/253,395
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-811-012-1

Query Match      100.0%; Score 397; DB 18; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CCTCGCTGGCTCCTGACCTGGAGCGGAGCGGCGGCGGCGGCGGGAAGCGCGGC 60
Db      13148  CCTCGCTGGCTCCTGACCTGGAGCGGAGCGGCGGCGGCGGCGGGAAGCGCGGC 13207

QY      61  CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTCCGGGGCCAGCGGGCTCCACAGT 120
Db      13208  CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTCCGGGGCCAGCGGGCTCCACAGT 13267

QY      121  GATTGCGGGGCACAGACGCCCGAGGACCGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 180
Db      13268  GATTGCGGGGCACAGACGCCCGAGGACCGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 13327

QY      181  GGGCACCCGCTCTGCGCCCTTACCTTCCAGTCCGCTCTCCGCGCGGACCCCGCCCG 240
Db      13328  GGGCACCCGCTCTGCGCCCTTACCTTCCAGTCCGCTCTCCGCGCGGACCCCGCCCG 13387

QY      241  TCCGACCCCTCCGGGTCCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db      13388  TCCGACCCCTCCGGGTCCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 13447

QY      301  CTTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Db      13448  CTTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 13507

QY      361  GGCACGTGGGAAGCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 397
Db      13508  GGCACGTGGGAAGCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 13544
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RESULT 12
US-10-840-455-1
; Sequence 1, Application US/10840455
; Publication No. US20050032094A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hagen, Gustav
; APPLICANT: Wick, Mareisa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
; TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
; FILE REFERENCE: LeA 32 805C1
; CURRENT APPLICATION NUMBER: US/10/840,455
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: PCT/EP98/08216
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/582,246
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: DE19757984.1
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 5126
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-455-1

Query Match      99.6%; Score 395.4; DB 19; Length 5126;
Best Local Similarity 99.7%; Pred. No. 1.9e-82;
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Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTCGTGGCGTCCCTGCACCTTGGAGCGGAGCGCGCGGGGAAAGCGCGC 60
Db 4727 CCCTCGTGGCGTCCCTGCACCTTGGAGCGGAGCGCGCGGGGAAAGCGCGC 4786

Qy 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGGGGCCAGCGCGGCTCCCAATG 120
Db 4787 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGGGGCCAGCGCGGCTCCCAATG 4846

Qy 121 GATTTCGGGGCACAGACCCCGGAGACCGCGCTTCCACGTGGCGAGGAGACTGGGGACCC 180
Db 4847 GATTTCGGGGCACAGACCCCGGAGACCGCGCTTCCACGTGGCGAGGAGACTGGGGACCC 4906

Qy 181 GGGCACCCCGTCTGCGCCCTTCACTTCAGCTTCGCGCTTCTCCGCGGAGACCCCGCGCG 240
Db 4907 GGGCACCCCGTCTGCGCCCTTCACTTCAGCTTCGCGCTTCTCCGCGGAGACCCCGCGCG 4966

Qy 241 TCCGACCCCTCCCGGGTCCCGCGGAGACCCCGCGCTTCCACGTGGCGAGGAGACTGGGGACCC 300
Db 4967 TCCGACCCCTCCCGGGTCCCGCGGAGACCCCGCGCTTCCACGTGGCGAGGAGACTGGGGACCC 5026

Qy 301 CCTTTCGGCGCGCGCGCGCTTCTCTCGCGGCGGAGTTTTCAGGAGCGCTGCTGCTGCT 360
Db 5027 CCTTTCGGCGCGCGCGCGCTTCTCTCGCGGCGGAGTTTTCAGGAGCGCTGCTGCTGCT 5086

Qy 361 GCGCACGTGGGAAGCCCTTGGCGCCCGCGCACCCCGCG 397
Db 5087 GCGCACGTGGGAAGCCCTTGGCGCCCGCGCACCCCGCG 5123

RESULT 13
US-10-840-455-3
; Sequence 3, Application US/10840455
; Publication No. US20050032094A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hagen, Gustav
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
; TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
; FILE REFERENCE: Lea 32 805C1
; CURRENT APPLICATION NUMBER: US/10/840,455
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: PCT/EP98/08216
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/582,246
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: DE19757984.1
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 11276
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-455-3

Query Match 99.6%; Score 395.4; DB 19; Length 11276;
Best Local Similarity 99.7%; Pred. No. 1.5e-82;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTCGTGGCGTCCCTGCACCTTGGAGCGGAGCGCGCGGGGAAAGCGCGC 60
Db 10877 CCCTCGTGGCGTCCCTGCACCTTGGAGCGGAGCGCGCGGGGAAAGCGCGC 10936

Qy 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGGGGCCAGCGCGGCTCCCAATG 120
Db 10937 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGGGGCCAGCGCGGCTCCCAATG 10996

Qy 121 GATTTCGGGGCACAGACCCCGGAGACCGCGCTTCCACGTGGCGAGGAGACTGGGGACCC 180

Db 10997 GATTTCGGGGCACAGACCCCGGAGACCGCGCTCCACAGTGGCGAGGAGACTGGGGACCC 11056

Qy 181 GGGCACCCCGTCTGCGCCCTTCACTTCAGCTTCGCGCTTCTCCGCGGAGACCCCGCGCG 240
Db 11057 GGGCACCCCGTCTGCGCCCTTCACTTCAGCTTCGCGCTTCTCCGCGGAGACCCCGCGCG 11116

Qy 241 TCCGACCCCTCCCGGGTCCCGCGGAGACCCCGCGCTTCCACGTGGCGAGGAGACTGGGGACCC 300
Db 11117 TCCGACCCCTCCCGGGTCCCGCGGAGACCCCGCGCTTCCACGTGGCGAGGAGACTGGGGACCC 11176

Qy 301 CCTTTCGGCGCGCGCGCTTCTCTCGCGGCGGAGTTTTCAGGAGCGCTGCTGCTGCT 360
Db 11177 CCTTTCGGCGCGCGCGCTTCTCTCGCGGCGGAGTTTTCAGGAGCGCTGCTGCTGCT 11236

Qy 361 GCGCACGTGGGAAGCCCTTGGCGCCCGCGCACCCCGCG 397
Db 11237 GCGCACGTGGGAAGCCCTTGGCGCCCGCGCACCCCGCG 11273

RESULT 14
US-10-840-455-43
; Sequence 43, Application US/10840455
; Publication No. US20050032094A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hagen, Gustav
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
; TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
; FILE REFERENCE: Lea 32 805C1
; CURRENT APPLICATION NUMBER: US/10/840,455
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: PCT/EP98/08216
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/582,246
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: DE19757984.1
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 26414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-455-43

Query Match 99.6%; Score 395.4; DB 19; Length 26414;
Best Local Similarity 99.7%; Pred. No. 1.2e-82;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTCGTGGCGTCCCTGCACCTTGGAGCGGAGCGCGCGGGGAAAGCGCGC 60
Db 10877 CCCTCGTGGCGTCCCTGCACCTTGGAGCGGAGCGCGCGGGGAAAGCGCGC 10936

Qy 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGGGGCCAGCGCGGCTCCCAATG 120
Db 10937 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGGGGCCAGCGCGGCTCCCAATG 10996

Qy 121 GATTTCGGGGCACAGACCCCGGAGACCGCGCTTCCACGTGGCGAGGAGACTGGGGACCC 180
Db 10997 GATTTCGGGGCACAGACCCCGGAGACCGCGCTTCCACGTGGCGAGGAGACTGGGGACCC 11056

Qy 181 GGGCACCCCGTCTGCGCCCTTCACTTCAGCTTCGCGCTTCTCCGCGGAGACCCCGCGCG 240
Db 11057 GGGCACCCCGTCTGCGCCCTTCACTTCAGCTTCGCGCTTCTCCGCGGAGACCCCGCGCG 11116

Qy 241 TCCGACCCCTCCCGGGTCCCGCGGAGACCCCGCGCTTCCACGTGGCGAGGAGACTGGGGACCC 300
Db 11117 TCCGACCCCTCCCGGGTCCCGCGGAGACCCCGCGCTTCCACGTGGCGAGGAGACTGGGGACCC 11176

Qy 301 CCTTTCGGCGCGCGCGCTTCTCTCGCGGCGGAGTTTTCAGGAGCGCTGCTGCTGCT 360

Db	11177	CTTTTCGGGGCCCGCCCTCTCTCGGCGGAGTTTTCAGGACGCGTGCCTCTGCT	11236
Qy	361	GCACAGCTGGGAAGCCCTGCCTCCCGCCACCCCGCG	397
Db	11237	GCACAGCTGGGAAGCCCTGCCTCCCGCCACCCCGCG	11273

RESULT 15

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US-09-733-294A-30
; Sequence 30, Application US/09733294A
; Patent No. US20020045588A1
GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Frasier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 05/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 30
; LENGTH: 51552
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)...(11492)
; OTHER INFORMATION: exon 1
; NAME/KEY: intron
; LOCATION: (11493)...(11596)
; OTHER INFORMATION: intron 1
; NAME/KEY: exon
; LOCATION: (11597)...(12950)
; OTHER INFORMATION: exon 2
; NAME/KEY: intron
; LOCATION: (12951)...(21566)
; OTHER INFORMATION: intron 2
; NAME/KEY: exon
; LOCATION: (21567)...(21762)
; OTHER INFORMATION: exon 3
; NAME/KEY: intron
; LOCATION: (21763)...(23851)
; OTHER INFORMATION: intron 3
; NAME/KEY: exon
; LOCATION: (23852)...(24032)
; OTHER INFORMATION: exon 4
; NAME/KEY: intron
; LOCATION: (24033)...(24719)
; OTHER INFORMATION: intron 4
; NAME/KEY: exon
; LOCATION: (24720)...(24899)
; OTHER INFORMATION: exon 5
; NAME/KEY: intron
; LOCATION: (24900)...(25393)
; OTHER INFORMATION: intron 5
; NAME/KEY: exon
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; LOCATION: (30195)...(30292)
; OTHER INFORMATION: exon 7
; NAME/KEY: intron
; LOCATION: (30293)...(31272)
; OTHER INFORMATION: intron 7
; NAME/KEY: exon
; LOCATION: (31273)...(31358)
; OTHER INFORMATION: exon 8

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Qy 241 TCCGACCCCTCCCGGTTCCCGGCCAGCCCCCTCCGGGCCCTCCAGCCCCCTCCCTT 300
 Db |||||
 11117 TCCGACCCCTCCCGGTTCCCGGCCAGCCCCCTCCGGGCCCTCCAGCCCCCTCCCTT 11176
 Qy 301 CCTTTCGGCGCCCGCCCTCTCCTCGCGGCCGAGTTTCAGGCAAGCGTGGTCTCTGCT 360
 Db |||||
 11177 CCTTTCGGCGCCCGCCCTCTCCTCGCGGCCGAGTTTCAGGCAAGCGTGGTCTCTGCT 11236
 Qy 361 GCGCACGTGGGAAGCCCTGGGCCCGGCCACCCCGCG 397
 Db |||||
 11237 GCGCACGTGGGAAGCCCTGGGCCCGGCCACCCCGCG 11273

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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	397	100.0	4321	4	US-09-402-181B-6
2	397	100.0	15418	4	US-09-783-203-1
3	397	100.0	15418	4	US-09-804-427A-1
4	397	100.0	15418	4	US-09-244-438-1
5	395.4	99.6	44952	4	US-09-749-016-12197
6	395.4	99.6	44960	4	US-09-949-016-17583
7	395.4	99.6	51552	4	US-09-733-294A-30
8	354.2	89.2	35871	4	US-09-956-335-2
9	354.2	89.2	35978	4	US-09-956-335-1
10	351	88.4	1677	4	US-09-956-335-3
11	341.8	86.1	4335	3	US-08-974-549A-6
12	341.8	86.1	4335	4	US-09-721-456-6
13	338.8	85.3	4200	4	US-08-912-951-6
14	298.2	75.1	314	4	US-09-916-510A-8
15	295	74.3	298	4	US-09-244-438-17
16	256.4	64.6	261	4	US-09-932-581-24
17	256.4	64.6	5928	4	US-09-932-581-25
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19	93.6	23.6	124	4	US-09-721-456-726
20	77	13.4	78	4	US-09-932-581-7
21	74	18.6	77	4	US-09-244-438-19
22	74	18.6	89	4	US-09-244-438-20
23	65.2	16.4	319	3	US-09-165-264-8
24	64.6	16.3	320	3	US-09-165-264-7
25	64	16.1	865	4	US-09-270-767-11042
26	63.2	15.9	320	3	US-09-165-264-14
27	62.2	15.7	320	3	US-09-165-264-13

C 28	62.2	15.7	14340	4	US-09-949-016-16972	Sequence 16972, A
C 29	62	15.6	318	3	US-09-165-264-12	Sequence 12, Appl
C 30	61.8	15.6	54779	4	US-09-949-001-27	Sequence 27, Appl
C 31	61.8	15.6	54780	4	US-09-949-001-39	Sequence 39, Appl
C 32	61.2	15.4	320	3	US-09-165-264-11	Sequence 11, Appl
C 33	60.2	15.2	8100	4	US-09-949-016-13460	Sequence 13460, A
C 34	60.2	15.2	8100	4	US-09-949-016-13461	Sequence 13461, A
C 35	58.6	14.8	7218	1	US-08-232-463-14	Sequence 14, Appl
C 36	58.2	14.7	393	4	US-09-107-433-1828	Sequence 1828, Ap
C 37	58.2	14.7	690	4	US-09-107-433-226	Sequence 226, App
C 38	58.2	14.7	795	4	US-09-107-433-195	Sequence 195, App
C 39	58.2	14.7	1536	4	US-09-107-433-301	Sequence 301, App
C 40	58.2	14.7	152331	3	US-09-128-155-16	Sequence 16, Appl
C 41	57.8	14.6	2561	4	US-09-616-289-48	Sequence 48, Appl
C 42	57.6	14.5	2376	4	US-09-023-655-932	Sequence 932, App
C 43	57.6	14.5	2404	3	US-08-945-771-1	Sequence 1, Appl
C 44	57.2	14.4	12001	1	US-08-458-568A-11	Sequence 11, Appl
C 45	57.2	14.4	670689	4	US-09-949-016-12505	Sequence 12505, A

ALIGNMENTS

RESULT 1
US-09-402-181B-6
; Sequence 6, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:

Qy 61 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTGCGGGCCAGGCGCGGCTCCCAAGT 120
Db 13208 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTGCGGGCCAGGCGCGGCTCCCAAGT 13267
Qy 121 GATTGCGGGGCACAGAGCCGAGGACCGGCTTCCACGTGCGGAGGACTGGGGACCC 180
Db 13268 GATTGCGGGGCACAGAGCCGAGGACCGGCTTCCACGTGCGGAGGACTGGGGACCC 13327
Qy 181 GGGACACCGTCTGCGCCCTTCCACCTTCCAGCTGCGGCTCCCTCCGCGGAGCCCGCCCG 240
Db 13328 GGGACACCGTCTGCGCCCTTCCACCTTCCAGCTGCGGCTCCCTCCGCGGAGCCCGCCCG 13387
Qy 241 TCCGACCCCTCCGCGGTCCGCGCCAGCCCTTCCGCGGCTCCCTCCAGCCCTCCCTT 300
Db 13388 TCCGACCCCTCCGCGGTCCGCGCCAGCCCTTCCGCGGCTCCCTCCAGCCCTCCCTT 13447
Qy 301 CCTTTCGCGGCGCGCCCTCTCTCGCGGCGGAGTTTTCAGGAGCGCTCGCTCTGCT 360
Db 13448 CCTTTCGCGGCGCGCCCTCTCTCGCGGCGGAGTTTTCAGGAGCGCTCGCTCTGCT 13507
Qy 361 GCGCAGCTGGGAAGCCCTGCGGCCCGCCAGCCCGCCCGCG 397
Db 13508 GCGCAGCTGGGAAGCCCTGCGGCCCGCCAGCCCGCCCGCG 13544

RESULT 4
US-09-244-438-1
; Sequence 1, Application US/09244438
; Patent No. 6777203
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; FILE OF INVENTION: Regulatory Sequences and Methods of Using
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/09/244, 438
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-09-244-438-1

Query Match 100.0%; Score 397; DB 4; Length 15418;
Best Local Similarity 100.0%; Pred. No. 3.2e-71;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGCTGGGTCCCTGACCCCTGGAGCGAGCGCGCGCGGGAGCGCGC 60
Db 13148 CCCTGCTGGGTCCCTGACCCCTGGAGCGAGCGCGCGCGGGAGCGCGC 13207
Qy 61 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTGCGGGCCAGGCGCGGCTCCCAAGT 120
Db 13208 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTGCGGGCCAGGCGCGGCTCCCAAGT 13267
Qy 121 GATTGCGGGGCACAGAGCCGAGGACCGGCTTCCACGTGCGGAGGACTGGGGACCC 180
Db 13268 GATTGCGGGGCACAGAGCCGAGGACCGGCTTCCACGTGCGGAGGACTGGGGACCC 13327
Qy 181 GGGACACCGTCTGCGCCCTTCCACCTTCCAGCTGCGGCTCCCTCCGCGGAGCCCGCCCG 240
Db 13328 GGGACACCGTCTGCGCCCTTCCACCTTCCAGCTGCGGCTCCCTCCGCGGAGCCCGCCCG 13387
Qy 241 TCCGACCCCTCCGCGGTCCGCGCCAGCCCTTCCGCGGCGCTCCCAAGCCTTCCCTT 300

Db 13388 TCCGACCCCTCCCGGGTCCCGGGCCAGAGCCCTTCCGAGCCCTCCAGAGCCCTTCCCTT 13447
Qy 301 CCTTTCGCGGCGCGCCCTTCTCTCGCGGCGGAGTTTTCAGGAGCGCTCGCTCTGCT 360
Db 13448 CCTTTCGCGGCGCGCCCTTCTCTCGCGGCGGAGTTTTCAGGAGCGCTCGCTCTGCT 13507
Qy 361 GCGCAGCTGGGAAGCCCTGCGGCCCGCCAGCCCGCCCGCG 397
Db 13508 GCGCAGCTGGGAAGCCCTGCGGCCCGCCAGCCCGCCCGCG 13544

RESULT 5
US-09-949-016-12197
; Sequence 12197, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12197
; LENGTH: 44952
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(44952)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12197

Query Match 99.6%; Score 395.4; DB 4; Length 44952;
Best Local Similarity 99.7%; Pred. No. 6.8e-71;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTGCTGGGTCCCTGACCCCTGGAGCGAGCGCGCGCGGGAGCGCGC 60
Db 1659 CCCTGCTGGGTCCCTGACCCCTGGAGCGAGCGCGCGGGAGCGCGC 1718
Qy 61 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGCTGTGCGGGCCAGGCGCGGCTCCCAAGT 120
Db 1719 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGCTGTGCGGGCCAGGCGCGGCTCCCAAGT 1778
Qy 121 GATTGCGGGGCACAGAGCCCGAGGACCGGCTTCCACGTGCGGAGGACTGGGGACCC 180
Db 1779 GATTGCGGGGCACAGAGCCCGAGGACCGGCTTCCACGTGCGGAGGACTGGGGACCC 1838
Qy 181 GGGACACCGTCTGCGCCCTTCCACCTTCCAGCTGCGGCTCCCTCCGCGGAGCCCGCCCG 240
Db 1839 GGGACACCGTCTGCGCCCTTCCACCTTCCAGCTGCGGCTCCCTCCGCGGAGCCCGCCCG 1898
Qy 241 TCCGACCCCTCCGCGGTCCCGCGCCAGCCCTTCCGCGGCTTCCCAAGCCTTCCCTT 300
Db 1899 TCCGACCCCTCCGCGGTCCCGCGCCAGCCCTTCCGCGGCTTCCCAAGCCTTCCCTT 1958
Qy 301 CCTTTCGCGGCGCGCCCTCTCTCGCGGCGGAGTTTTCAGGAGCGCTCGCTCTGCT 360
Db 1959 CCTTTCGCGGCGCGCCCTCTCTCGCGGCGGAGTTTTCAGGAGCGCTCGCTCTGCT 2018
Qy 361 GCGCAGCTGGGAAGCCCTTGGGCCCGCCAGCCCGCCCGCG 397
Db 2019 GCGCAGCTGGGAAGCCCTTGGGCCCGCCAGCCCGCCCGCG 2055

NAME/KEY: exon
LOCATION: (37885)...(38073)
OTHER INFORMATION: exon 11
NAME/KEY: intron
LOCATION: (38074)...(41874)
OTHER INFORMATION: intron 11
NAME/KEY: exon
LOCATION: (41875)...(42001)
OTHER INFORMATION: exon 12
NAME/KEY: intron
LOCATION: (42002)...(42881)
OTHER INFORMATION: intron 12
NAME/KEY: exon
LOCATION: (42882)...(42943)
OTHER INFORMATION: exon 13
NAME/KEY: intron
LOCATION: (42944)...(46129)
OTHER INFORMATION: intron 13
NAME/KEY: exon
LOCATION: (46130)...(46254)
OTHER INFORMATION: exon 14
NAME/KEY: intron
LOCATION: (46255)...(47035)
OTHER INFORMATION: intron 14
NAME/KEY: exon
LOCATION: (47036)...(47173)
OTHER INFORMATION: exon 15
NAME/KEY: intron
LOCATION: (47174)...(47709)
OTHER INFORMATION: intron 15
NAME/KEY: exon
LOCATION: (47710)...(50544)
OTHER INFORMATION: exon 16
US-09-956-335-2

Query Match 99.6%; Score 395.4; DB 4; Length 51552;

Best Local Similarity 99.7%; Pred. No. 6.8e-71;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCTCGCTGGGCTCCCTGCACCTGGGAGCGGAGCGCGCGGGCGGGAAGCGCGGC 60
DB 10877 CCCTCGCTGGGCTCCCTGCACCTGGGAGCGGAGCGCGCGGGCGGGAAGCGCGGC 10936

QY 61 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTGCGGGGCGCAGCGCGGCTCCCACTG 120
DB 10937 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTGCGGGGCGCAGCGCGGCTCCCACTG 10996

QY 121 GATTCGGGGCACAGACGCCCGGAGCGCGGCTTCCACGTGCGGAGGAGCTGGGGACCC 180
DB 10997 GATTCGGGGCACAGACGCCCGGAGCGCGGCTTCCACGTGCGGAGGAGCTGGGGACCC 11056

QY 181 GGGCACCGCTCTGCGGCTTCCACCTTCCAGCTCCGCGGCTTCCGCGGAGCGCGGCGCG 240
DB 11057 GGGCACCGCTCTGCGGCTTCCACCTTCCAGCTCCGCGGCTTCCGCGGAGCGCGGCGCG 11116

QY 241 TCCGACCCCTCCCGGGTCCCGGCGGAGCGCGGCTTCCGCGGCTTCCGCGGAGCGCGGCGCG 300
DB 11117 TCCGACCCCTCCCGGGTCCCGGCGGAGCGCGGCTTCCGCGGCTTCCGCGGAGCGCGGCGCG 11176

QY 301 CCTTTCCGGGCGCGCGCTCTCTCTGCGGGCGGAGTTTCAGGACGCGCTGCGTCTGCT 360
DB 11177 CCTTTCCGGGCGCGCGCTCTCTCTGCGGGCGGAGTTTCAGGACGCGCTGCGTCTGCT 11236

QY 361 GCGCAGTGGGAAGCCCTGGCGCGGCGCGGCGCGCGCGCG 397
DB 11237 GCGCAGTGGGAAGCCCTGGCGCGGCGCGGCGCGCGCGCG 11273

RESULT 8

US-09-956-335-2/c
; Sequence 2, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:

APPLICANT: WOLD, William
APPLICANT: TOTH, Karoly
APPLICANT: KUPPASWAMI, Mohan
APPLICANT: DORONIN, Konstantin
TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
FILE REFERENCE: 16153-8394
CURRENT APPLICATION NUMBER: US/09/956.335
CURRENT FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 35871
TYPE: DNA
ORGANISM: Adenovirus
US-09-956-335-2

Query Match 89.2%; Score 354.2; DB 4; Length 35871;

Best Local Similarity 99.2%; Pred. No. 1.2e-62;
Matches 356; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTCGCTGGGCTCCCTGCACCTGGGAGCGGAGCGCGGGCGGGAAGCGCGGC 60
DB 34385 CCCTCGCTGGGCTCCCTGCACCTGGGAGCGGAGCGCGGGCGGGAAGCGCGGC 34326

QY 61 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTGCGGGGCGCAGCGCGGCTCCCACTG 120
DB 34325 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTGCGGGGCGCAGCGCGGCTCCCACTG 34266

QY 121 GATTCGGGGCACAGACGCCCGGAGCGCGGCTTCCAGTGGCGGAGGAGCTGGGGACCC 180
DB 34265 GATTCGGGGCACAGACGCCCGGAGCGCGGCTTCCAGTGGCGGAGGAGCTGGGGACCC 34206

QY 181 GGGCACCGCTCTGCGGCTTCCACCTTCCAGCTCCGCGGCTTCCGCGGAGCGCGGCGCG 240
DB 34205 GGGCACCGCTCTGCGGCTTCCACCTTCCAGCTCCGCGGCTTCCGCGGAGCGCGGCGCG 34146

QY 241 TCCGACCCCTCCCGGGTCCCGGCGGAGCGCGGCTTCCGCGGCTTCCGCGGAGCGCGGCGCG 300
DB 34145 TCCGACCCCTCCCGGGTCCCGGCGGAGCGCGGCTTCCGCGGCTTCCGCGGAGCGCGGCGCG 34086

QY 301 CCTTTCCGGGCGCGCGCTCTCTCTGCGGGCGGAGTTTCAGGACGCGCTGCGTCTGCT 359
DB 34085 CCTTTCCGGGCGCGCGCTCTCTCTGCGGGCGGAGTTTCAGGACGCGCTGATTACTGC 34027

RESULT 9

US-09-956-335-1/c
; Sequence 1, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:

APPLICANT: WOLD, William
APPLICANT: TOTH, Karoly
APPLICANT: KUPPASWAMI, Mohan
APPLICANT: DORONIN, Konstantin
TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
FILE REFERENCE: 16153-8394
CURRENT APPLICATION NUMBER: US/09/956.335
CURRENT FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 35978
TYPE: DNA
ORGANISM: Adenovirus
US-09-956-335-1

Query Match 89.2%; Score 354.2; DB 4; Length 35978;

Best Local Similarity 99.2%; Pred. No. 1.2e-62;
Matches 356; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTCGCTGGGCTCCCTGCACCTGGGAGCGGAGCGCGGGCGGGAAGCGCGGC 60

Db 34492 CCCTCGCTGGCTCCCTGACCTGGAGCGAGCGCGCGCGGGAAGCGCGGC 34433
Qy 61 CCAGACCCCGCGGTCGCGCCGAGAGCTGCGCTGTCGCGGCGAGCGCGGCTCCAGTG 120
Db 34432 CCAGACCCCGCGGTCGCGCCGAGAGCTGCGCTGTCGCGGCGAGCGCGGCTCCAGTG 34373
Qy 121 GATTGCGGGCACAGACGCCAGGACCGCGCTTCCACAGCTGCGGAGGACTGGGAGCC 180
Db 34372 GATTGCGGGCACAGACGCCAGGACCGCGCTTCCACAGCTGCGGAGGACTGGGAGCC 34313
Qy 181 GGGACACCGCTCTCGGCTTACCTTCCAGCTCCGCTTCTCGCGGCGAGACCCCGCGG 240
Db 34312 GGGACACCGCTCTCGGCTTACCTTCCAGCTCCGCTTCTCGCGGCGAGACCCCGCGG 34253
Qy 241 TCCCGACCCCTCCCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 34252 TCCCGACCCCTCCCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 34193
Qy 301 CCTTTCCGGCGCGCGCGCTCTCTCGCGGCGGCGGCTTTCAGGACGCGTCTGCTGC 359
Db 34192 CCTTTCCGGCGCGCGCGCTCTCTCGCGGCGGCGGCTTTCAGGACGCGTCTGCTGC 34134

RESULT 10
US-09-956-335-3/c
; Sequence 3, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:
; APPLICANT: WOLD, William
; APPLICANT: TOTH, Karoly
; APPLICANT: KUPPASWAMI, Mohan
; APPLICANT: DORONIN, Konsantin
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
; TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
; FILE REFERENCE: 16153-8394
; CURRENT APPLICATION NUMBER: US/09/956,335
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1677
; TYPE: DNA
; ORGANISM: Adenovirus
US-09-956-335-3

Query Match 88.4%; Score 351; DB 4; Length 1677;
Best Local Similarity 100.0%; Pred. No. 5.2e-62; Mismatches 0; Indels 0; Gaps 0;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTCGCTGGCTCCCTGACCTGGAGCGGAGCGCGCGCGCGGCGGGAAGCGCGGC 60
Db 353 CCCTCGCTGGCTCCCTGACCTGGAGCGGAGCGCGCGCGCGGCGGGAAGCGCGGC 294
Qy 61 CCAGACCCCGGTCGCGCCGAGAGCTGCGCTGTCGCGGCGAGCGCGGCTCCAGTG 120
Db 293 CCAGACCCCGGTCGCGCCGAGAGCTGCGCTGTCGCGGCGAGCGCGGCTCCAGTG 234
Qy 121 GATTGCGGGCACAGACGCCAGGACCGCGCTTCCACAGCTGCGGAGGACTGGGAGCC 180
Db 233 GATTGCGGGCACAGACGCCAGGACCGCGCTTCCACAGCTGCGGAGGACTGGGAGCC 174
Qy 181 GGGACACCGCTCTCGGCTTACCTTCCAGCTCCGCTTCTCGCGGCGGACCCCGCGG 240
Db 173 GGGACACCGCTCTCGGCTTACCTTCCAGCTCCGCTTCTCGCGGCGGACCCCGCGG 114
Qy 241 TCCGACCCCTCCCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 113 TCCGACCCCTCCCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 54
Qy 301 CCTTTCCGGCGCGCGCTCTCTCGCGGCGGCGGCTTTCAGGACGCGTGC 351
Db 53 CCTTTCCGGCGCGCGCTCTCTCGCGGCGGCGGCTTTCAGGACGCGTGC 3

RESULT 11
US-08-974-549A-6
; Sequence 6, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4335 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..4335
; OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2715..2818
; OTHER INFORMATION: /note= "intron 1"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 4173..4326
; OTHER INFORMATION: /note= "intron 2"
; US-08-974-549A-6

Query Match      86.1%; Score 341.8; DB 3; Length 4335;
Best Local Similarity 97.3%; Pred. No. 3.7e-60;
Matches 390; Conservative 0; Mismatches 7; Indels 4; Gaps 4;

Qy 1 CCCTCGCTGGGTCCTCTGCACCTGGAGCGGCGCGCGCGGCGGGAAGCGCGC 60
Db 2095 CCCTCGCTGGGTCCTCTGCACCTGGAGCGGCGCGCGCGGCGGGAAGCGCGC 2154

Qy 61 CCAGACCCCGGTCGCGCGGAGCAGCTGCGCTGTGCGGCGCCAGGCGCGGCTCCCACTG 120
Db 2155 CCAGACCCCGGTCGCGCGGAGCAGCTGCGCTGTGCGGCGCCAGGCGCGGCTCCCACTG 2214

Qy 121 GATTGCGGGC-ACAGACGCCAGACCGCGCTTCCACGTGCGGCGGAGGACTGGGACC 179
Db 2215 GATTGCGGGC-ACAGACGCCAGACCGCGCTTCCACGTGCGGCGGAGGACTGGGACC 2274

Qy 180 CGGCGACCGCTCTGCGGCTTCCACCTTCCAGTCCGCTCTGCGGCGGG-ACCCGCGCC 238
Db 2275 CGGCGACCGCTCTGCGGCTTCCACCTTCCAGTCCGCTCTGCGGCGGGAACCCGCGCC 2334

Qy 239 GGTCCG-ACCCCTTCCGGTCCCGCGCCAGCCGCTTCCGCGGCTTCCAGCCGCTTCC 297
Db 2335 GGTCCGAAACCTTCCCGGTCGCGGCGCCAGCGGCTTCCGCGGCTTCCAGCCGCTTCC 2394

Qy 298 GTTCC-TTTTCCGCGGCGCGGCTTCCGCGGCGGAGTTTCCAGGAGGCTGCGTCC 356
Db 2395 GTTCC-TTTTCCGCGGCGCGGCTTCCGCGGCGGAGTTTCCAGGAGGCTGCGTCC 2454

Qy 357 TGCTGCGCAGTGGGAAGCCCTGCGGCGCGGCGCACCCCGCG 397
Db 2455 TGCTGCGCAGTGGGAAGCCCTGCGGCGCGGCGCACCCCGCG 2495

RESULT 12
US-09-721-456-6
; Sequence 6, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;               Lingner, Joachim
;               Nakamura, Toru
;               Chapman, Karen B.
;               Morin, Gregg B.
;               Harley, Calvin B.
;               Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721.456
; FILING DATE: 22-Nov. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974.549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US/08/724.643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US/08/844.419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US/08/846.017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US/08/851.843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US/08/854.050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US/08/911.312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US/08/912.951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US/08/915.503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..4335
; OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2715..2818
; OTHER INFORMATION: /note= "intron 1"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 4173..4326
; OTHER INFORMATION: /note= "intron 2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-721-456-6

Query Match      86.1%; Score 341.8; DB 4; Length 4335;
Best Local Similarity 97.3%; Pred. No. 3.7e-60;
Matches 390; Conservative 0; Mismatches 7; Indels 4; Gaps 4;

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Db 2095 CCCTCGCTGGGTCCTCTGCACCTGGAGCGGCGCGCGGCGGGAAGCGCGC 2154

Qy 61 CCAGACCCCGGTCGCGCGGAGCAGCTGCGCTGTGCGGCGCCAGGCGCGGCTCCCACTG 120
Db 2155 CCAGACCCCGGTCGCGCGGAGCAGCTGCGCTGTGCGGCGCCAGGCGCGGCTCCCACTG 2214

Qy 121 GATTGCGGGC-ACAGACGCCAGACCGCGCTTCCACGTGCGGCGGAGGACTGGGACC 179
Db 2215 GATTGCGGGC-ACAGACGCCAGACCGCGCTTCCACGTGCGGCGGAGGACTGGGACC 2274

Qy 180 CGGCGACCGCTCTGCGGCTTCCACCTTCCAGTCCGCTCTGCGGCGGG-ACCCGCGCC 238
Db 2275 CGGCGACCGCTCTGCGGCTTCCACCTTCCAGTCCGCTCTGCGGCGGGAACCCGCGCC 2334

Qy 239 GGTCCG-ACCCCTTCCGGTCCCGCGCCAGCCGCTTCCGCGGCTTCCAGCCGCTTCC 297
Db 2335 GGTCCGAACCTTCCCGGTCGCGGCGCCAGCGGCTTCCGCGGCTTCCAGCCGCTTCC 2394

Qy 298 GTTCC-TTTTCCGCGGCGCGGCTTCCGCGGCGGAGTTTCCAGGAGGCTGCGTCC 356
Db 2395 GTTCC-TTTTCCGCGGCGCGGCTTCCGCGGCGGAGTTTCCAGGAGGCTGCGTCC 2454

Qy 357 TGCTGCGCAGTGGGAAGCCCTGCGGCGCGGCGCACCCCGCG 397
Db 2455 TGCTGCGCAGTGGGAAGCCCTGCGGCGCGGCGCACCCCGCG 2495
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QY 180 CCGGACACCGCTCTGCGCCCTTACCTTCCAGTTCGGCCTTCCCGCGCGG-ACCCCGCGCC 238
Db 2275 CCGGACACCGCTCTGCGCCCTTACCTTCCAGTTCGGCCTTCCCGCGGAGACCCCGCC 2334
QY 239 CGTCCCG-ACCCCTCCCGGGTCCCGGCGGACGCGCCCTCCCGGCGCTCCACGCGCTCC 297
Db 2335 CGTCCCGAACCTTCCCGGGTCCCGGCGGACGCGCCCTCCCGGCGCATCCACGCGCTCC 2394
QY 298 CTTCC-TTTCGGGCGCGCGCCCTCTCTCCGCGGCGGAGTTTCAGGACAGCGCTCGCTCC 356
Db 2395 GTTCTCTTTTCCCGGCGCGCGCCCTCTCTCCGCGGCGGAGTTTCAGGACAGCGCTCGCTCC 2454
QY 357 TCGTGGCAGTGGGAAGCCCTGGCGCGCGCGCGCACCCCGCG 397
Db 2455 TCGTGGCAGTGGGAAGCCCTGGCGCGCGCGCGCACCCCGCG 2495

RESULT 13
US-08-912-951-6
; Sequence 6, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-912-951-6
Query Match 85.3%; Score 338.8; DB 4; Length 4200;
Best Local Similarity 96.2%; Pred. No. 1.5e-59;
Matches 379; Conservative 0; Mismatches 12; Indels 3; Gaps 3;
QY 7 CTGGGCTCCCTGCACCCCTGGGAGCGCGGCGCGGCGGGAAGCGCGGCCAGAC 66
Db 1919 CTGGGCTCCCTGCACCCCTGGGAGCGCGGCGCGGCGGGAAGCGCGGCCATAC 1978
QY 67 CCCGGGTCCGCGCGG-AGCAGCTGCGCTGTGCGGGCCAGGCGCGGCTCCCAAGTGGATT 125
Db 1979 CCCGGGTCCGCGCGGAGAGAGCTGCGCTGTGCGGGCCAGGCGCGGCTCCCAAGTGGATT 2038
QY 126 GCGGACACAGACGCGCGGCGCTTCCACGTGGCGGAGGAGTGGGGACCCCGCGGCA 185
Db 2039 GCGGACACAGACGCGCGGCGCTTCCACGTGGCGGAGGAGTGGGGACCCCGCGGCA 2098
QY 186 CCGTCTCCGCGCTTCACTTCCAGCTCGGCTCTCTCGGCGGAGACCCCGCGCTCCCG 245
Db 2099 CCGTCTCCGCGCTTCACTTCCAGCTCGGCTCTCTCGGCGGAGACCCCGCGCTCCCG 2158
QY 246 ACCCTCCCGGCTCCCGGCGCGCGCTCCCGGCGCTCCCGGCGCTCCCGCTTCC- 304
Db 2159 AACCTTCCAGTCCCGGCGCGCGCTTCCCGGCGCTTCCCGGCGCTTCCCGCTTCC 2218
QY 305 TCCGCGCGCGCGCTCTCC-TCGCGGCGCGAGTTTCAGGACGCGCTGCGTCTGCTGCG 363
Db 2219 TCCGCGCGCGCGCTCTCTTCCGCGCGCGAGTTTCAGGACGCGCTGCGTCTGCTGCG 2278
QY 364 CACGTGGGAAGCCCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 397
Db 2279 CACGTGGGAAGCCCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2312
RESULT 14
US-09-916-510A-8
; Sequence 8, Application US/09916510A
; Patent No. 6544507
; GENERAL INFORMATION:
; APPLICANT: IGGO, RICHARD D.
; APPLICANT: BRUNORI, MICHELE A.
; TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
; FILE REFERENCE: 604-596
; CURRENT APPLICATION NUMBER: US/09/916.510A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: GB 9906815.7
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-916-510A-8
Query Match 75.1%; Score 298.2; DB 4; Length 314;
Best Local Similarity 98.7%; Pred. No. 2e-51;
Matches 311; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 83 AGCAGTCCGCTGTGCGGCGCGCGCGCTCCCAAGTGGATTTCGCGGCGCACAGCGCCA 142

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Job time : 130.15 secs

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Db      181  GGCCACAGCCCTCCCGGG-CTTCCAGCCCGCCCTTCTTCTTCCGCGGGCCCGGCCCTCT 239
QY      323  CTTCCGCGGGAGTTTTCAGCAGCGCTGCGTCTGCTGCGCACCTGGGAAAGCCCTGGCC 382
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QY      383  CCGGCCACCCCGCG 397
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RESULT 15

US-09-244-438-17

; Sequence 17, Application US/09244438

; Patent No. 6777203

; GENERAL INFORMATION:

; APPLICANT: Morin, Gregg B.

; APPLICANT: Lichtsteiner, Serge

; APPLICANT: Vasserot, Alain

; APPLICANT: Adams, Robert R.

; APPLICANT: Geron Corporation

; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional

; FILE OF INVENTION: Regulatory Sequences and Methods of Using

; FILE REFERENCE: 019/246P

; CURRENT APPLICATION NUMBER: US/09/244,438

; CURRENT FILING DATE: 1999-02-04

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 298

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Human TERT promoter

US-09-244-438-17

Query Match

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Matches 295; Conservativeness 100.0%; Pred. No. 8.7e-51;

Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61  CGGAGGAGTGGGAGACCGGGACCGGTCCTGCGGCTTCCAGTCCAGTCCGCTCCTC 120
QY      223  CGCGGGACCGGCGCCCGGTCGCGACCCCTCGGGGTCCCGGCGGCGGCGGCGGCGG 282
Db      121  CGCGGGACCGGCGCCCGGTCGCGACCCCTCGGGGTCCCGGCGGCGGCGGCGGCGG 180
QY      283  CTCCAGCGGCTCCCGCTTCTTCCGCGGCGGCGGCGGCTTCTCTCGGGGAGTTCAG 342
Db      181  CTCCAGCGGCTCCCGCTTCTTCCGCGGCGGCGGCGGCTTCTCTCGGGGAGTTCAG 240
QY      343  GCAGCGCTGCGTCTGCTGCGGACCGTGGGAGCCCTGGCCCGGCGGCGGCGGCGG 397
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 04:29:03 ; Search time 416.17 Seconds
(without alignment)
5647.064 Million cell updates/sec

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Perfect score: 397
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : N_Geneseq_16Dec04.*
- 1: Geneseq1980s.*
 - 2: Geneseq1990s.*
 - 3: Geneseq2000s.*
 - 4: Geneseq2001as.*
 - 5: Geneseq2001bs.*
 - 6: Geneseq2002as.*
 - 7: Geneseq2002bs.*
 - 8: Geneseq2003as.*
 - 9: Geneseq2003bs.*
 - 10: Geneseq2003cs.*
 - 11: Geneseq2003ds.*
 - 12: Geneseq2004as.*
 - 13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	397	100.0	397	6	ABs98658 Human TER
2	397	100.0	408	13	ADR73423 Human tel
3	397	100.0	902	13	ADR73427 Human m-h
4	397	100.0	3962	4	AaH41091 Telomeras
5	397	100.0	15418	3	AaA63785 Nucleotid
6	397	100.0	15418	6	AaL38601 Human TER
7	397	100.0	15418	6	ABs54997 Lambda cl
8	397	100.0	15418	6	AALJ8595
9	397	100.0	15418	10	ADC21253 Lambda cl
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13	376.4	94.8	378	8	ACC47272 CEA gene
c 14	354.2	89.2	35871	6	AAD27972 Recombina
c 15	354.2	89.2	35978	6	AAD27971 Recombina
c 16	351	88.4	1677	6	AAD27973 Human tel
17	341.8	86.1	4335	2	AAV16979 Human tel
18	328.6	82.8	454	11	ADN00285 Tumour-sp
19	298.2	75.1	314	3	AA94134 Telomeras
c 20	273.8	69.0	4356	6	ABU92335 Chemicall

21	260.4	65.6	327	6	AAL55438
22	260.4	65.6	327	12	ADI80429
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27	256.4	64.6	295	8	ABV75306
28	256.4	64.6	295	10	ABZ23897
29	256.4	64.6	5928	6	ABK12707
30	244	61.5	245	6	ABs98659
c 31	244	61.5	955	6	ABs98580
c 32	216.4	54.5	240	10	ABZ23898
c 33	212.2	53.5	1404	6	AAD22344
c 34	199.8	50.3	403	6	ABs98583
35	181.2	45.6	4356	6	ABL92334
36	144	36.3	144	8	ABZ79850
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40	77	19.4	78	8	ABZ79851
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c 42	70.6	17.8	3163	10	ADC87060
c 43	68.6	17.3	629	13	ACN54594
c 44	68.2	17.2	3133	10	ADC86738
c 45	67.8	17.1	588	13	ACN54596

ALIGNMENTS

RESULT 1

ABs98658
ID ABs98658 standard; DNA; 397 BP.

XX AC ABs98658;

XX DT 17-DEC-2002 (first entry)

XX DE Human TERT promoter sequence #1.

XX KW Virus; viral vector; adenoviral nucleic acid backbone; breast cancer;
KW inverted terminal repeat; ITR; termination signal sequence; lung cancer;
KW E2F responsive promoter; adenoviral packaging signal; prostate cancer;
KW neoplastic condition; colon cancer; cytostatic; immunostimulant;
KW gene therapy; human; TERT; promoter; ds.

XX OS Homo sapiens

XX PN MO200267861-A2

XX PD 06-SEP-2002.

XX PF 22-FEB-2002; 2002WO-US005300.

XX PR 23-FEB-2001; 2001US-0270922P.

XX PR 01-JUN-2001; 2001US-0295037P.

XX PR 14-JAN-2002; 2002US-0348670P.

XX PA (NOVS) NOVARTIS PHARMA AG.

XX PI Ennist DL, Forry-Schaudies S, Gorziglia M, Hallenbeck PL, Hay CW;

XX PI Jakubczak JL, Kaleko M, Ryan PC, Stewart DA, Xie Y, Connelly S;

XX PI Police SR, Clarke L, Phipps S, Cheng C;

XX DR WPI, 2002-706950/76.

XX PT Recombinant viral vector comprising an adenoviral nucleic acid backbone,

XX PT useful for treating neoplastic disorders such as lung, breast, prostate

XX PS or colon cancer.

XX PS Claim 11; Page 21; 226pp; English.

XX CC The present invention relates to a new recombinant viral vector

CC comprising an adenoviral nucleic acid backbone, where the backbone
CC comprises in sequential order, a left inverted terminal repeat (ITR), a
CC termination signal sequence, an E2F responsive promoter which is operably
CC linked to a gene essential for replication of the recombinant viral
CC vector, an adenoviral packaging signal and a right ITR. The methods and
CC compositions of the present invention are useful for treating a
CC neoplastic condition such as lung, breast, prostate or colon cancer. The
CC viral vectors are useful in studying methods of killing neoplastic cells
CC in vitro or in animal models. The present nucleic acid sequence
CC represents a human TERT promoter of the invention
XX
SQ Sequence 397 BP; 35 A; 186 C; 127 G; 49 T; 0 U; 0 Other;
Query Match 100.0%; Score 397; DB 6; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.9e-56;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTCGCTGGCGTCCCTGTCACCTTGGAGCGCGAGCGCGCGGGGAGCGCGGC 60
DB 1 CCCTCGCTGGCGTCCCTGTCACCTTGGAGCGCGAGCGCGCGGGGAGCGCGGC 60
QY 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGCGGGCCAGGCCGGGCTCCAGTG 120
DB 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGCGGGCCAGGCCGGGCTCCAGTG 120
QY 121 GATTTCGGGGCACAGACGCCCGGCTTCCACAGTGGCGGAGGACTGGGGACCC 180
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QY 181 GGGACACCGCTCTGCGCCCTTACCTTCCAGTCCGCTCTCTCGCGCGGACCCCGCCG 240
DB 181 GGGACACCGCTCTGCGCCCTTACCTTCCAGTCCGCTCTCTCGCGCGGACCCCGCCG 240
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DB 241 TCCGACCCCTTCCGGGTCCCGGCGGAGCCCTTCCAGTCCGCGGCTCCAGCCCTTCCCTT 300
QY 301 CTTTTCGGCGGCCCGCCCTCTCTCGCGGCGGAGTTTCAGGCAGCGGTGCGTCTCTGCT 360
DB 301 CTTTTCGGCGGCCCGCCCTCTCTCGCGGCGGAGTTTCAGGCAGCGGTGCGTCTCTGCT 360
QY 361 GCGCAGCTGGGAGCCCTGCGCCCGCGGACCCCGCG 397
DB 361 GCGCAGCTGGGAGCCCTGCGCCCGCGGACCCCGCG 397
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ID ADR73423 standard; DNA; 408 BP.
XX
AC ADR73423;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human telomerase reverse transcriptase (hTERT) gene promoter sequence.
XX
KW ds; cytosstatic; gene therapy; transcriptional regulatory sequence;
KW human telomere reverse transcriptase; hTERT; promoter;
KW c-Myc binding site; SPl binding site; cancer.
XX
OS Homo sapiens.
XX
PN WO2004076668-A1.
XX
PD 10-SEP-2004.
XX
PF 27-FEB-2004; 2004WO-KR000427.
XX
PR 27-FEB-2003; 2003KR-00012364.
XX
PA (YUNC/) YUN C.
PA (KIMJ/) KIM J.
XX

PI Yun C, Kim J, Yang J;
XX
DR WPI; 2004-653423/63.
XX
PT New transcriptional regulatory sequence with a human telomere reverse
PT transcriptase promoter, useful for treating cancer, e.g. stomach, lung,
PT ovarian, liver, pancreatic, bladder, colon, cervical, breast, brain, or
PT head and neck cancer.
XX
PS Disclosure; SEQ ID NO 1; 130pp; English.
XX
CC The invention relates to a transcriptional regulatory sequence with a
CC human telomere reverse transcriptase (hTERT) promoter linked to a
CC nucleotide sequence comprising one or more c-Myc binding sites and/or one
CC or more SPl binding sites. The transcriptional regulatory sequence and
CC composition are useful for treating cancer, e.g. stomach, lung, ovarian,
CC liver, bronchogenic, nasopharyngeal, laryngeal, pancreatic, bladder,
CC colon, cervical, breast, brain, or head and neck cancer. This sequence
CC corresponds to the wild type human telomerase reverse transcriptase
CC (hTERT) promoter sequence used to generate the novel sequence of the
CC invention.
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SQ Sequence 408 BP; 35 A; 190 C; 132 G; 51 T; 0 U; 0 Other;
Query Match 100.0%; Score 397; DB 13; Length 408;
Best Local Similarity 100.0%; Pred. No. 2.9e-56;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 12 CCCTCGCTGGGTCCCTGTCACCTGGAGCGCGAGCGCGGGGAGCGCGGC 71
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DB 72 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGCGGGCCAGGCCGGGCTCCAGTG 131
QY 121 GATTTCGGGGCACAGACGCCCGGCTTCCAGTTCGCGGCGGAGGACTGGGGACCC 180
DB 132 GATTTCGGGGCACAGACGCCCGGCTTCCAGTTCGCGGCGGAGGACTGGGGACCC 191
QY 181 GGGACACCGCTCTGCGCCCTTACCTTCCAGTTCGCGGCGGAGCCCGCCG 240
DB 192 GGGACACCGCTCTGCGCCCTTACCTTCCAGTTCGCGGCGGAGCCCGCCG 251
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DB 252 TCCGACCCCTTCCGGGTCCCGGCGGAGCCCTTCCAGTTCGCGGCGGAGCCCTTCCCTT 311
QY 301 CTTTTCGGCGGCCCGCCCTCTCTCGCGGCGGAGTTTCAGGCAGCGGTGCGTCTCTGCT 360
DB 312 CTTTTCGGCGGCCCGCCCTCTCTCGCGGCGGAGTTTCAGGCAGCGGTGCGTCTCTGCT 371
QY 361 GCGCAGCTGGGAGCCCTGCGCCCGCGGACCCCGCG 397
DB 372 GCGCAGCTGGGAGCCCTGCGCCCGCGGACCCCGCG 408
RESULT 3
ADR73427
ID ADR73427 standard; DNA; 902 BP.
XX
AC ADR73427;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human m-hTERT gene promoter sequence.
XX
KW ds; cytosstatic; gene therapy; transcriptional regulatory sequence;
KW human telomere reverse transcriptase; hTERT; promoter;
KW c-Myc binding site; SPl binding site; cancer.
XX
OS Homo sapiens.
XX

PH FT protein_bind Location/Qualifiers
173..178 /tag= a
FT /bound_moiety= "c-Myc protein"
FT /tag= b
FT /bound_moiety= "Spl transcription factor"
FT /tag= c
FT /bound_moiety= "Spl transcription factor"
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FT /tag= n
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PN WO2004076668-A1.
XX 10-SEP-2004.
XX 27-FEB-2004; 2004WO-KR000427.
XX 27-FEB-2003; 2003KR-00012364.
XX (YUNC/) YUN C.
XX (KIMJ/) KIM J.
XX Yun C, Kim J, Yang J;
XX WPI; 2004-653423/63.
XX New transcriptional regulatory sequence with a human telomere reverse
PT transcripase promoter, useful for treating cancer, e.g. stomach, lung,
PT ovarian, liver, pancreatic, bladder, colon, cervical, breast, brain, or
PT head and neck cancer.
XX Claim 6; SEQ ID NO 13; 130pp; English.
XX The invention relates to a transcriptional regulatory sequence with a
CC human telomere reverse transcriptase (hTERT) promoter linked to a
CC nucleotide sequence comprising one or more c-Myc binding sites and/or one
CC or more Spl binding sites. The transcriptional regulatory sequence and
CC composition are useful for treating cancer, e.g. stomach, lung, ovarian,
CC liver, bronchogenic, nasopharyngeal, laryngeal, pancreatic, bladder,
CC colon, cervical, breast, brain, or head and neck cancer. This sequence

CC corresponds to the modified human telomerase reverse transcriptase
CC (hTERT) promoter sequence containing the extra c-Myc and Spl binding site
CC sequences.
XX
SQ Sequence 902 BP; 103 A; 388 C; 282 G; 129 T; 0 U; 0 Other;
Query Match 100.0%; Score 397; DB 13; Length 902;
Best Local Similarity 100.0%; Pred. No. 2.5e-56;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTCGCTGGCGTCCCTGCACCTGGGAGCGCGAGCGCGCGCGCGGGAAGCGCGGC 60
Db 18 CCCTCGCTGGCGTCCCTGCACCTGGGAGCGCGAGCGCGCGCGGGAAGCGCGGC 77
Qy 61 CCAGACCCCGGGTCCCGCCCGGAGCAGCTGCGTGTGCGGGGCCAGCGCGCTCCCAATG 120
Db 78 CCAGACCCCGGGTCCCGCCCGGAGCAGCTGCGTGTGCGGGGCCAGCGCGCTCCCAATG 137
Qy 121 GATTGCGGGGCACAGACGCCCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 180
Db 138 GATTGCGGGGCACAGACGCCCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 197
Qy 181 GGGCACCCTGCTCCCTTCCACCTTCCAGCTCCGCGCTTCCCTCCGCGGACCCCGCCCG 240
Db 198 GGGCACCCTGCTCCCTTCCACCTTCCAGCTCCGCGCTTCCCTCCGCGGACCCCGCCCG 257
Qy 241 TCCGACCCCTTCCCGGGTCCCGGCCAGCCCTTCCGCGGCCCTCCAGCCCTTCCCTTT 300
Db 258 TCCGACCCCTTCCCGGGTCCCGGCCAGCCCTTCCGCGGCCCTCCAGCCCTTCCCTTT 317
Qy 301 CCTTTCCGCGGCCCGCGCTTCCCTTCCGCGGCCAGTTTCAAGGAGCGCTGGTCTCTCT 360
Db 318 CCTTTCCGCGGCCCGCGCTTCCCTTCCGCGGCCAGTTTCAAGGAGCGCTGGTCTCTCT 377
Qy 361 GCGCAGCTGGGAGCGCTTCCGCGGCCAGCCCGCGGCCAGCCCGCGCG 397
Db 378 GCGCAGCTGGGAGCGCTTCCGCGGCCAGCCCGCGGCCAGCCCGCGCG 414
RESULT 4
AAH41091
ID AAH41091 standard; DNA; 3962 BP.
XX
AC AAH41091;
XX
DT 29-AUG-2001 (first entry)
XX
DE Telomerase reverse transcriptase (TERT) DNA.
XX
KW Phenotype switch molecule; phenotype-related gene battery;
KW gene localisation; telomere reverse transcriptase; TERT; ds.
XX
OS Unidentified.
XX
PN WO200138515-A1.
XX
PD 31-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-CN000427.
XX
PR 19-NOV-1999; 99CN-00121466.
XX
PA (BIAN/) BIAN X.
XX
PI Bian X;
XX
DR WPI; 2001-367684/38.
XX
PT Isolating phenotype switch molecules and phenotype-related gene batteries
PT from complex genomes of higher animals and plants, useful e.g. in gene
PT localization and classification analysis.
XX
PS Example 7; Page 27-29; 35pp; Chinese.

XX This invention relates to a method for isolating phenotype switch
CC molecules and phenotype-related gene batteries from complex genomes of
CC higher animals and plants. The method is useful in gene localisation and
CC classification analysis, studying gene development networks and function
CC networks, and designing drugs based on regulatory sequences of the
CC phenotypes for disease treatment. The present sequence represents DNA
CC encoding a telomere reverse transcriptase (TERT), which is used in an
CC example illustrating the use of the method of the invention
XX
SQ Sequence 3962 BP; 782 A; 1157 C; 1113 G; 910 T; 0 U; 0 Other;
Query Match 100.0%; Score 397; DB 4; Length 3962;
Best Local Similarity 100.0%; Pred. No. 2e-56;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTCTGCTGGGTCCTCTGACCTCTGGAGCGGAGCGGCGGGGAGCGCGGC 60
DB 3529 CCTCTGCTGGGTCCTCTGACCTCTGGAGCGGAGCGGCGGGGAGCGCGGC 3588
QY 61 CCAGACCCCGGGTCCCGCGGAGCAGCTCGCTGTGGGGCCAGGCCGGGCTCCCAAGTG 120
DB 3589 CCAGACCCCGGGTCCCGCGGAGCAGCTCGCTGTGGGGCCAGGCCGGGCTCCCAAGTG 3648
QY 121 GATTGCGGGGCACAGAGCCCGGAGCGGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 180
DB 3649 GATTGCGGGGCACAGAGCCCGGAGCGGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 3708
QY 181 GGGCACCCTGCTGCTGCTTCACTTCCAGCTCCGCTCTCCGCGCGGACCCCGCGCG 240
DB 3709 GGGCACCCTGCTGCTGCTTCACTTCCAGCTCCGCTCTCCGCGCGGACCCCGCGCG 3768
QY 241 TCCGACCCCTCCCGGGTCCCGCGGAGCAGCTCCGCTGTGGGGCCAGGCCGGGCTCCCGCTT 300
DB 3769 TCCGACCCCTCCCGGGTCCCGCGGAGCAGCTCCGCTGTGGGGCCAGGCCGGGCTCCCGCTT 3828
QY 301 CCTTTCCGCGGGCCCGGCTCTCTCTGCGGGCGGAGTTTCAGGACGCGTCTGCTGCT 360
DB 3829 CCTTTCCGCGGGCCCGGCTCTCTCTGCGGGCGGAGTTTCAGGACGCGTCTGCTGCT 3888
QY 361 GCGCAGCTGGGAGACCTGCGGCCCGGCGCACCCCGCGG 397
DB 3889 GCGCAGCTGGGAGACCTGCGGCCCGGCGCACCCCGCGG 3925

RESULT 5
AA63785
ID AAA63785 standard; DNA; 15418 BP.

AC AAA63785;

DT 04-DEC-2000 (first entry)

XX Nucleotide sequence of the human TERT promoter and gene from pGRN142.

XX Telomerase reverse transcriptase; TERT; promoter; telomerase complex;
XX telomere length; hyperplastic disease; cancer; oncolytic virus;
XX cis-acting transcriptional control sequence; viral replication;
XX cell proliferation; aging; immunological disorder; infertility; ss.

OS Homo sapiens.

XX WO200046355-A2

PN 10-AUG-2000.

XX 04-FEB-2000; 2000WO-US003104.

XX 04-FEB-1999; 99US-00244438.

XX (GERO-) GERON CORP.

XX Morin GB, Lichtsteiner S, Vasserot A, Adams R, Cardoza LM;

PI Lebkowski JS;

XX WPI; 2000-532898/48.

XX New polynucleotides comprising cis-acting transcriptional control
PT sequences, e.g. promoter sequence, of telomerase reverse transcriptase
PT genes, useful in the treatment of cancer.

XX Claim 9; Page 58-61; 63pp; English.

XX The present sequence represents the human telomerase reverse
CC transcriptase (TERT) promoter and gene. TERT is part of the telomerase
CC complex responsible for maintaining telomere length and increasing
CC replicative capacity of progenitor cells. Telomerase activity is turned
CC off in mature differentiated cells, but is turned back on again in
CC hyperplastic diseases, including many cancers. The polynucleotide
CC comprises cis-acting transcriptional control sequences, e.g. promoter
CC sequences. These promoter sequences are used to produce oncolytic viruses,
CC in which a toxin or genetic element essential for viral replication is
CC placed under the control of a TERT promoter. As a result, the virus
CC replicates preferentially in cells expressing TERT, and selectively lyses
CC cancer cells. The oncolytic viruses are useful for treating cancer in
CC humans or animals. The TERT promoter sequences are useful in the
CC treatment of cancer and other diseases of cell proliferation such as
CC degenerative and aging processes and diseases of aging, immunological
CC disorders, or infertility

XX Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 397; DB 3; Length 15418;

Best Local Similarity 100.0%; Pred. No. 1.6e-56;

Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTGCTGGGTCCTCTGACCTCTGGAGCGGAGCGGCGGGGAGCGCGGC 60

DB 13148 CCTCTGCTGGGTCCTCTGACCTCTGGAGCGGAGCGGCGGGGAGCGCGGC 13207

QY 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGGGGCCAGGCCGGGCTCCCAAGTG 120

DB 13208 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGGGGCCAGGCCGGGCTCCCAAGTG 13267

QY 121 GATTGCGGGGCACAGAGCCCGGAGCGGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 180

DB 13268 GATTGCGGGGCACAGAGCCCGGAGCGGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 13327

QY 181 GGGCACCCTGCTGCTGCTTCACTTCCAGCTCCGCTCTCCGCGCGGACCCCGCGCG 240

DB 13328 GGGCACCCTGCTGCTGCTTCACTTCCAGCTCCGCTCTCCGCGCGGACCCCGCGCG 13387

QY 241 TCCGACCCCTCCCGGGTCCCGCGGAGCAGCTCCGCTGTGGGGCCAGGCCGGGCTCCCGCTT 300

DB 13388 TCCGACCCCTCCCGGGTCCCGCGGAGCAGCTCCGCTGTGGGGCCAGGCCGGGCTCCCGCTT 13447

QY 301 CCTTTCCGCGGGCCCGGCTCTCTCTGCGGGCGGAGTTTCAGGACGCGTCTGCTGCT 360

DB 13448 CCTTTCCGCGGGCCCGGCTCTCTCTGCGGGCGGAGTTTCAGGACGCGTCTGCTGCT 13507

QY 361 GCGCAGCTGGGAGACCTGCGGCCCGGCGCACCCCGCGG 397

DB 13508 GCGCAGCTGGGAGACCTGCGGCCCGGCGCACCCCGCGG 13544

RESULT 6

AAAL38601

ID AAL38601 standard; DNA; 15418 BP.

XX AAL38601;

XX 16-AUG-2002 (first entry)

XX Human TERT promoter and upstream sequence.

XX Cytostatic; glycosyltransferase; tumour; cell-surface carbohydrate;

KW tissue specific; transcriptional control element; cancer cell;
XX gene therapy; human TERT; telomerase reverse transcriptase; ds.

OS Homo sapiens.

PN WO200242468-A2.

XX 30-MAY-2002.

XX 26-NOV-2001; 2001WO-US044306.

XX 27-NOV-2000; 2000US-025339SP.

XX (GERO-) GERON CORP.

XX Schiff MJ;

XX WPI; 2002-479954/51.

XX New polynucleotide encoding glycosyltransferase enzymes including histo
PT blood group transferase useful for treating conditions associated with
PT hyperproliferation, such as cancers and other neoplasias.

PS Claim 9; Page 17-20; 49pp; English.

XX The invention relates to a polynucleotide comprising an encoding sequence
CC for a glycosyltransferase, under control of a heterologous tumour
CC specific or tissue specific transcriptional control element, where
CC expression of the polynucleotide in a human cell causes the cell to
CC express a cell-surface carbohydrate determinant to which some or all
CC humans have a naturally occurring antibody. The polynucleotide of the
CC invention is useful for killing cancer cells and for preparing a
CC medicament for the treatment of cancer. The polynucleotide sequence of
CC the invention can be used to treat disorders by gene therapy. This
CC polynucleotide sequence represents the human TERT (telomerase reverse
CC transcriptase) promoter and upstream sequence related to the invention
XX Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 397; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTCGTGGCGTCCCTGACACCTGGAGCGAGCGCGCGCGCGGGAAGCGCGC 60
Db 13148 CCCTCGTGGCGTCCCTGACACCTGGAGCGAGCGCGCGCGGGAAGCGCGC 13207
QY 61 CCAGACCCCGGTCGCGCGGAGCAGCTGCGCTGCGGCGCAGCGCGGCTCCACTG 120
Db 13208 CCAGACCCCGGTCGCGCGGAGCAGCTGCGCTGCGGCGCAGCGCGGCTCCACTG 13267
QY 121 GATTCCGGGACAGACGCGCCAGGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 180
Db 13268 GATTCCGGGACAGACGCGCCAGGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 13327
QY 181 GGGCACCCGTCGTCGCCCTTACCTTCCAGCTCCGCTTCCGCGCGGACCCGCCCGC 240
Db 13328 GGGCACCCGTCGTCGCCCTTACCTTCCAGCTCCGCTTCCGCGCGGACCCGCCCGC 13387
QY 241 TCCGACCCCTCCCGGTCGCGCGGACCGCGCCCTCCGGGCTCCGACCCCTCCCTT 300
Db 13388 TCCGACCCCTCCCGGTCGCGCGGACCGCGCCCTCCGGGCTCCGACCCCTCCCTT 13447
QY 301 CTTTTCGGGCGCGCGCCCTCTCTCGCGGCGGAGTTTCAGGACGCGTGGTCTCTGCT 360
Db 13448 CTTTTCGGGCGCGCGCCCTCTCTCGCGGCGGAGTTTCAGGACGCGTGGTCTCTGCT 13507
QY 361 GGCACGTTGGGAAGCCCTGCGCCCGGCGCACACCCCGCG 397
Db 13508 GGCACGTTGGGAAGCCCTGCGCCCGGCGCACACCCCGCG 13544

RESULT 7

ABS54997

ID ABS54997; standard; DNA; 15418 BP.

XX AC ABS54997;

XX 10-DEC-2002 (first entry)

XX Lambda clone containing human TERT genomic insert.

XX Telomerase reverse transcriptase; TERT; replication-conditional virus;
KW adenovirus replication gene; cancer cell; lung; pancreatic cancer;
KW medulloblastoma; cervical carcinoma; fibrosarcoma; osteosarcoma;
KW cytotoxic; replication defective adenovirus vector; congenital defect;
KW proinflammatory; antiinflammatory; heterologous effector gene; cancer therapy; cytostatic; gene therapy; lambda clone; human; ds.

XX Bacteriophage lambda.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT misc_feature 1..43

FT /tag= a

FT /note= "From Lambda clone"

FT misc_feature 44..15375

FT /tag= b

FT /note= "Human telomerase reverse transcriptase (hTERT) sequence including the hTERT promoter and upstream sequence"

FT misc_feature 15376..15418

FT /tag= c

FT /note= "From Lambda clone"

XX WO200253760-A2.

XX 11-JUL-2002.

XX 17-DEC-2001; 2001WO-US048785.

XX 18-DEC-2000; 2000US-0256418P.

XX (GERO-) GERON CORP.

XX Irving JM, Lebkowski JS;

XX WPI; 2002-723123/78.

XX Novel replication-conditional virus useful for cytotoxicity of target cells
PT e.g. cancer cells and preparing a medicament for treating cancer,
PT comprises heterologous replication element in an adenovirus-based construct.

XX Claim 11; Page 26-29; 32pp; English.

XX The present invention relates to a new replication-conditional virus with
CC a genome comprising adenovirus replication genes and one or more
CC heterologous gene(s) that functionally replaces one or more adenovirus
CC gene(s) required for replication or assembly of the virus. The invention
CC is useful for killing a cancer cell (such as lung, pancreatic cancer,
CC medulloblastoma, cervical carcinoma, fibrosarcoma or osteosarcoma),
CC killing a cell expressing TERT (telomerase reverse transcriptase), and in
CC preparing a medicament for treating cancer and a condition associated
CC with increased expression of TERT in affected cells, in a subject. The
CC invention is also useful for cytotoxicity of specific target cells. The
CC invention is further useful for producing replication defective
CC adenovirus vector which is useful for transient expression of a
CC heterologous therapeutic gene to correct a congenital defect, introducing
CC proinflammatory or antiinflammatory activity, enhancing telomerase
CC function, and delivering heterologous effector genes that induce killing
CC of the transduced cells. The invention is more safe for use in cancer
CC therapy. The present nucleic acid sequence represents the human TERT
CC sequence contained within a lambda clone sequence of the invention

SQ	Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;	
XX	Query Match 100.0%; Score 397; DB 6; Length 15418;	
PT	Best Local Similarity 100.0%; Pred. No. 1.6e-56;	
PT	Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		
PS	Example 9; Page 62-66; 67pp; English.	
XX	The invention relates to a system for depleting a cell population of	
CC	undifferentiated stem cells, by introducing nucleic acids of structure P-	
CC	X, where X is a nucleic acid encoding product that is lethal to a cell in	
CC	which it is expressed; or renders a cell in which it is expressed	
CC	susceptible to the lethal effect of an external agent, and P is a	
CC	transcriptional control element causing X to be preferentially expressed	
CC	in the undifferentiated stem cells. The system is used for depleting a	
CC	cell population (preferably, human embryonic stem cells) of	
CC	undifferentiated stem cells. A population of differentiated cells is	
CC	useful in regenerative medicine, and for preparing antibodies and cDNA	
CC	libraries that are specific for a differentiated phenotype. The cell	
CC	populations are also useful for drug screening and therapeutic	
CC	applications. The differentiated cells are useful for tissue	
CC	reconstitution or regeneration in a human patient in need of treatment.	
CC	The cells are administered in a manner that permits to graft to the	
CC	intended tissue side and reconstitute or regenerate the functionally	
CC	deficient area. The neural progenitor cells are useful for treating acute	
CC	or chronic damage to the nerve system e.g. epilepsy, stroke, ischaemia,	
CC	Huntington's disease, Parkinson's disease, multiple sclerosis,	
CC	leukodystrophies, neuritis, etc. The hepatocytes and hepatocyte	
CC	precursors are useful for assessing animal models for ability to repair	
CC	liver damage. The cardiomyocyte population is useful for assessing animal	
CC	models for cryoinjury, regenerating cardiac muscle and to treat	
CC	insufficient cardiac function. This polynucleotide sequence represents	
CC	the DNA of plasmid pGRN144 containing the human hTERT gene relating to	
CC	the invention	
XX		
SQ	Sequence 15418 BP; 4519 A; 3797 C; 3764 G; 3338 T; 0 U; 0 Other;	
XX	Query Match 100.0%; Score 397; DB 6; Length 15418;	
XX	Best Local Similarity 100.0%; Pred. No. 1.6e-56;	
XX	Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		
QY	1 CCCTCGCTGGCGTCCCTGCACCTTGGAGAGCGGCGCGGGGGAAGCGCGGC 60	1 CCCTCGCTGGCGTCCCTGCACCTTGGAGAGCGGCGCGGGGGAAGCGCGGC 60
DB	13148 CCCTCGCTGGCGTCCCTGCACCTTGGAGAGCGGCGCGGGGGAAGCGCGGC 13207	13148 CCCTCGCTGGCGTCCCTGCACCTTGGAGAGCGGCGCGGGGGAAGCGCGGC 13207
QY	61 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTCCGGGCGCAGCGCGGCTCCCAAGTG 120	61 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTCCGGGCGCAGCGCGGCTCCCAAGTG 120
DB	13208 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTCCGGGCGCAGCGCGGCTCCCAAGTG 13267	13208 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTCCGGGCGCAGCGCGGCTCCCAAGTG 13267
QY	121 GATTCCGGGGCACAGACGCCAGGACCGCGTTTCCACGTGGCGGAGGACTGGGGACCC 180	121 GATTCCGGGGCACAGACGCCAGGACCGCGTTTCCACGTGGCGGAGGACTGGGGACCC 180
DB	13268 GATTCCGGGGCACAGACGCCAGGACCGCGTTTCCACGTGGCGGAGGACTGGGGACCC 13327	13268 GATTCCGGGGCACAGACGCCAGGACCGCGTTTCCACGTGGCGGAGGACTGGGGACCC 13327
QY	181 GGGCACCCGCTCTGCGCCCTTACCTTCAGCTCCGCGCTCTCCGCGCGACCCCGCCCG 240	181 GGGCACCCGCTCTGCGCCCTTACCTTCAGCTCCGCGCTCTCCGCGCGACCCCGCCCG 240
DB	13328 GGGCACCCGCTCTGCGCCCTTACCTTCAGCTCCGCGCTCTCCGCGCGACCCCGCCCG 13387	13328 GGGCACCCGCTCTGCGCCCTTACCTTCAGCTCCGCGCTCTCCGCGCGACCCCGCCCG 13387
QY	241 TCCCGACCCCTCCCGGGTCCCGCGCCAGCCCTTCCGGGCGCTCCCAAGCCCTCCCTTT 300	241 TCCCGACCCCTCCCGGGTCCCGCGCCAGCCCTTCCGGGCGCTCCCAAGCCCTCCCTTT 300
DB	13388 TCCCGACCCCTCCCGGGTCCCGCGCCAGCCCTTCCGGGCGCTCCCAAGCCCTCCCTTT 13447	13388 TCCCGACCCCTCCCGGGTCCCGCGCCAGCCCTTCCGGGCGCTCCCAAGCCCTCCCTTT 13447
QY	301 CTTTTCGCGGCGCCCGCCCTCTCTCTCGGCGCGAGTTTTCAGGCAGCGTCTGCTCT 360	301 CTTTTCGCGGCGCCCGCCCTCTCTCTCGGCGCGAGTTTTCAGGCAGCGTCTGCTCT 360
DB	13448 CTTTTCGCGGCGCCCGCCCTCTCTCTCGGCGCGAGTTTTCAGGCAGCGTCTGCTCT 13507	13448 CTTTTCGCGGCGCCCGCCCTCTCTCTCGGCGCGAGTTTTCAGGCAGCGTCTGCTCT 13507
QY	361 GCGCACGTTGGGAGCCCTGGCCCGCGGACCCCGCGG 397	361 GCGCACGTTGGGAGCCCTGGCCCGCGGACCCCGCGG 397
DB	13508 GCGCACGTTGGGAGCCCTGGCCCGCGGACCCCGCGG 13544	13508 GCGCACGTTGGGAGCCCTGGCCCGCGGACCCCGCGG 13544
XX		
RESULT 8		
AAL38595		
ID	AAL38595 standard; DNA; 15418 BP.	
XX		
AC	AAL38595;	
XX		
DT	16-AUG-2002 (first entry)	
XX		
DE	DNA of plasmid pGRN144 containing human hTERT gene.	
XX		
KW	Anticonvulsant; cerebroprotective; vasotropic; nootropic; stem cell;	
KW	neuroprotective; antiparkinsonian; antiinflammatory; undifferentiated;	
KW	cardiant; transcriptional control element; human embryonic; tissue graft;	
KW	regenerative medicine; tissue reconstitution; neural progenitor cell;	
KW	nerve system; epilepsy; stroke; ischaemia; Huntington's disease;	
KW	Parkinson's disease; multiple sclerosis; leukodystrophy; neuritis;	
KW	hepatocyte; liver damage; cardiomyocyte; cryoinjury; cardiac muscle;	
KW	pGRN144; human hTERT gene; chimeric; db.	
XX		
OS	Homo sapiens.	
OS	Unidentified.	
OS	Chimeric.	
XX		
PN	WO200242445-A2.	
XX		
PD	30-MAY-2002.	
XX		
PF	26-NOV-2001; 2001WO-US044309.	
XX		
PR	27-NOV-2000; 2000US-0253357P.	
PR	27-NOV-2000; 2000US-0253443P.	
PR	13-FEB-2001; 2001US-00783203.	
XX		
PA	(GERO-) GERON CORP.	
XX		
PI	Gold JD, Lebowski JS;	
XX		
DR	WPI; 2002-479952/51.	

XX		
PT	Depleting a cell e.g., human embryonic stem cell population of	
PT	undifferentiated stem cells (UC) for use in regenerative medicine	
PT	comprises genetically altering UC in a population to express nucleic acid	
PT	encoding a lethal product.	
XX		
PS	Example 9; Page 62-66; 67pp; English.	
XX	The invention relates to a system for depleting a cell population of	
CC	undifferentiated stem cells, by introducing nucleic acids of structure P-	
CC	X, where X is a nucleic acid encoding product that is lethal to a cell in	
CC	which it is expressed; or renders a cell in which it is expressed	
CC	susceptible to the lethal effect of an external agent, and P is a	
CC	transcriptional control element causing X to be preferentially expressed	
CC	in the undifferentiated stem cells. The system is used for depleting a	
CC	cell population (preferably, human embryonic stem cells) of	
CC	undifferentiated stem cells. A population of differentiated cells is	
CC	useful in regenerative medicine, and for preparing antibodies and cDNA	
CC	libraries that are specific for a differentiated phenotype. The cell	
CC	populations are also useful for drug screening and therapeutic	
CC	applications. The differentiated cells are useful for tissue	
CC	reconstitution or regeneration in a human patient in need of treatment.	
CC	The cells are administered in a manner that permits to graft to the	
CC	intended tissue side and reconstitute or regenerate the functionally	
CC	deficient area. The neural progenitor cells are useful for treating acute	
CC	or chronic damage to the nerve system e.g. epilepsy, stroke, ischaemia,	
CC	Huntington's disease, Parkinson's disease, multiple sclerosis,	
CC	leukodystrophies, neuritis, etc. The hepatocytes and hepatocyte	
CC	precursors are useful for assessing animal models for ability to repair	
CC	liver damage. The cardiomyocyte population is useful for assessing animal	
CC	models for cryoinjury, regenerating cardiac muscle and to treat	
CC	insufficient cardiac function. This polynucleotide sequence represents	
CC	the DNA of plasmid pGRN144 containing the human hTERT gene relating to	
CC	the invention	
XX		
SQ	Sequence 15418 BP; 4519 A; 3797 C; 3764 G; 3338 T; 0 U; 0 Other;	
XX	Query Match 100.0%; Score 397; DB 6; Length 15418;	
XX	Best Local Similarity 100.0%; Pred. No. 1.6e-56;	
XX	Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		
QY	1 CCCTCGCTGGCGTCCCTGCACCTTGGAGAGCGGCGCGGGGGAAGCGCGGC 60	1 CCCTCGCTGGCGTCCCTGCACCTTGGAGAGCGGCGCGGGGGAAGCGCGGC 60
DB	13148 CCCTCGCTGGCGTCCCTGCACCTTGGAGAGCGGCGCGGGGGAAGCGCGGC 13207	13148 CCCTCGCTGGCGTCCCTGCACCTTGGAGAGCGGCGCGGGGGAAGCGCGGC 13207
QY	61 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTCCGGGCGCAGCGCGGCTCCCAAGTG 120	61 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTCCGGGCGCAGCGCGGCTCCCAAGTG 120
DB	13208 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTCCGGGCGCAGCGCGGCTCCCAAGTG 13267	13208 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTCCGGGCGCAGCGCGGCTCCCAAGTG 13267
QY	121 GATTCCGGGGCACAGACGCCAGGACCGCGTTTCCACGTGGCGGAGGACTGGGGACCC 180	121 GATTCCGGGGCACAGACGCCAGGACCGCGTTTCCACGTGGCGGAGGACTGGGGACCC 180
DB	13268 GATTCCGGGGCACAGACGCCAGGACCGCGTTTCCACGTGGCGGAGGACTGGGGACCC 13327	13268 GATTCCGGGGCACAGACGCCAGGACCGCGTTTCCACGTGGCGGAGGACTGGGGACCC 13327
QY	181 GGGCACCCGCTCTGCGCCCTTACCTTCAGCTCCGCGCTCTCCGCGCGACCCCGCCCG 240	181 GGGCACCCGCTCTGCGCCCTTACCTTCAGCTCCGCGCTCTCCGCGCGACCCCGCCCG 240
DB	13328 GGGCACCCGCTCTGCGCCCTTACCTTCAGCTCCGCGCTCTCCGCGCGACCCCGCCCG 13387	13328 GGGCACCCGCTCTGCGCCCTTACCTTCAGCTCCGCGCTCTCCGCGCGACCCCGCCCG 13387
QY	241 TCCCGACCCCTCCCGGGTCCCGCGCCAGCCCTTCCGGGCGCTCCCAAGCCCTCCCTTT 300	241 TCCCGACCCCTCCCGGGTCCCGCGCCAGCCCTTCCGGGCGCTCCCAAGCCCTCCCTTT 300
DB	13388 TCCCGACCCCTCCCGGGTCCCGCGCCAGCCCTTCCGGGCGCTCCCAAGCCCTCCCTTT 13447	13388 TCCCGACCCCTCCCGGGTCCCGCGCCAGCCCTTCCGGGCGCTCCCAAGCCCTCCCTTT 13447
QY	301 CTTTTCGCGGCGCCCGCCCTCTCTCTCGGCGCGAGTTTTCAGGCAGCGTCTGCTCT 360	301 CTTTTCGCGGCGCCCGCCCTCTCTCTCGGCGCGAGTTTTCAGGCAGCGTCTGCTCT 360
DB	13448 CTTTTCGCGGCGCCCGCCCTCTCTCTCGGCGCGAGTTTTCAGGCAGCGTCTGCTCT 13507	13448 CTTTTCGCGGCGCCCGCCCTCTCTCTCGGCGCGAGTTTTCAGGCAGCGTCTGCTCT 13507
QY	361 GCGCACGTTGGGAGCCCTGGCCCGCGGACCCCGCGG 397	361 GCGCACGTTGGGAGCCCTGGCCCGCGGACCCCGCGG 397
DB	13508 GCGCACGTTGGGAGCCCTGGCCCGCGGACCCCGCGG 13544	13508 GCGCACGTTGGGAGCCCTGGCCCGCGGACCCCGCGG 13544
XX		
RESULT 9		
ADC21253		
ID	ADC21253 standard; DNA; 15418 BP.	

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XX AC ADC21253;
XX DT 18-DEC-2003 (first entry)
XX DE Lambda clone (lambdaGphi5) containing human TERT DNA.
XX KW Viral vector; heterologous control element; gene expression;
XX KW human telomerase reverse transcriptase; hTERT; tumour specific gene;
XX KW cell death; transcriptional control element;
XX KW human telomerase RNA component; hTR; cancer cell; liver cancer;
XX KW prostate cancer; muscle cancer; neural cell cancer; lung cancer;
XX KW pancreatic cancer; medulloblastoma; cervical carcinoma; fibrosarcoma;
XX KW osteosarcoma; lambda clone; lambdaGphi5; human; ds.
XX OS Synthetic.
XX OS Homo sapiens.
XX OS Bacteriophage lambda.
XX XX US2003099616-A1.
XX PD 29-MAY-2003.
XX PF 25-JUL-2002; 2002US-00206447.
XX XX 25-JUL-2001; 2001US-0308029P.
XX PA (IRVI/) IRVING J M.
XX PA (KARP/) KARP D B.
XX PA (SCHI/) SCHIFF J M.
XX PI Irving JM, Karpf DB, Schiff JM;
XX WPI; 2003-730140/69.
XX DR
XX PT New dual specificity vectors driven by the telomerase promoter, useful
XX PT for killing or slowing the growth of tumor cells, or for treating cancer,
XX PT e.g. liver cancer, prostate cancer, lung cancer, or pancreatic cancer.
XX PS Example 1; Page 13-20; 25pp; English.
XX CC The present invention relates to a viral vector comprising first and
XX CC second genes controlled by heterologous control elements, where the first
XX CC gene is preferentially expressed in cells expressing human telomerase
XX CC reverse transcriptase (hTERT), and another gene under the control of a
XX CC heterologous transcriptional control element for a tissue or tumour
XX CC specific gene other than TERT, and where transduction of the vector into
XX CC a mammalian cell expressing TERT causes the death of the cell or its
XX CC progeny. In particular, the second gene may be under the control of a
XX CC transcriptional control element for a tissue specific gene selected from
XX CC albumin, alpha-fetoprotein, prostate-specific antigen, mitochondrial
XX CC creatine kinase, myelin basic protein, glial fibrillary acidic protein,
XX CC and neuron-specific enolase. The second gene may be under the control of
XX CC a transcriptional control element for a human telomerase RNA component
XX CC (hTR). The vector of the invention is useful for killing a cancer cell,
XX CC or treating a subject for a condition associated with increased
XX CC expression of TERT in affected cells. The vector is also useful in the
XX CC preparation of a medicament for treatment of a condition associated with
XX CC increased expression of TERT, particularly cancer, and especially liver
XX CC cancer, prostate cancer, muscle cancer, neural cell cancer, lung cancer,
XX CC pancreatic cancer, medulloblastoma, cervical carcinoma, fibrosarcoma, and
XX CC osteosarcoma. The present sequence represents a lambda clone
XX CC (lambdaGphi5) containing human TERT DNA.
XX SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 397; DB 10; Length 15418;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-56;
XX Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 CCCTCGCTGGCTCCCTGCACCCCTGGAGCGCGCGCGCGCGGAGCGCGGC 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||
XX 13148 CCCTCGCTGGCTCCCTGCACCCCTGGAGCGCGCGCGCGCGGAGCGCGGC 13207
```

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Oy 61 CCAGACCCCGGGTCCGCCCGGAGCAGCTGGCTGTTCGGGGCCAGGCCGGGCTCCCAAGT 120
Db 13208 CCAGACCCCGGGTCCGCCCGGAGCAGCTGGCTGTTCGGGGCCAGGCCGGGCTCCCAAGT 13267
Oy 121 GATTTCGGGGCACAGAGCCCGCAGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 180
Db 13268 GATTTCGGGGCACAGAGCCCGCAGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 13327
Oy 181 GGGCACCCGCTCTGCCCGCTTCCACGTTCAGCTCCGCGCTCTCCCGGGGAGACCCGCGCCG 240
Db 13328 GGGCACCCGCTCTGCCCGCTTCCACGTTCAGCTCCGCGCTCTCCCGGGGAGACCCGCGCCG 13387
Oy 241 TCCCGACCCCTCCCGGGTCCCGGCGCCAGCCCTTCCGCGCCCTCCAGGCCCTTCCCTT 300
Db 13388 TCCCGACCCCTCCCGGGTCCCGGCGCCAGCCCTTCCGCGCCCTCCAGGCCCTTCCCTT 13447
Oy 301 CCTTTCCGCGCGCCCGCGCTCTCTCCGCGGCGGAGTTTCAGGCGAGCGCTCGCTCCTGCT 360
Db 13448 CCTTTCCGCGCGCCCGCGCTCTCTCTCGCGGCGGAGTTTCAGGCGAGCGCTCGCTCCTGCT 13507
Oy 361 GCGCACGTGGGAGCCCTTGGCCCGCGCACCCCGCGCG 397
Db 13508 GCGCACGTGGGAGCCCTTGGCCCGCGCACCCCGCGCG 13544

RESULT 10
ADI33422
ID ADI33422 standard; DNA; 455 BP.
XX AC ADI33422;
XX DT 22-APR-2004 (first entry)
XX DE Human telomerase promoter (hTERT) DNA SeqID 4.
XX KW human telomerase promoter; human; El; E1A; IRES; ElB; anticancer;
XX KW cell death; cancer; cytostatic; ds.
XX OS Homo sapiens.
XX PN WO2004005511-A1.
XX PD 15-JAN-2004.
XX PF 07-JUL-2003; 2003WO-JP008573.
XX PR 08-JUL-2002; 2002JP-00198941.
XX PA (KANS-) KANSAI TECHNOLOGY LICENSING ORG CO LTD.
XX PA (FUJI/) FUJIWARA T.
XX PA (TANA/) TANAKA N.
XX PA (KYOS/) KYO S.
XX PI Fujiwara T, Tanaka N, Kyo S, Shirakiya Y, Kawashima T;
XX WPI; 2004-099391/10.
XX PT Polynucleotide comprising a human telomerase promoter and an El gene for
XX PT treating cancer.
XX PS Example 1; SEQ ID NO 4; 34pp; Japanese.
XX CC This invention relates to a novel polynucleotide comprising a human
XX CC telomerase promoter and at least one viral El gene. Specifically, the El
XX CC genes are E1A, IRES and E1B and the human telomerase promoter is
XX CC polynucleotide and an anticancer agent that replicates efficiently in
XX CC tumour cells and causing cell death. As such, it can be used for the
XX CC treatment of cancer, in particular cancer of the stomach, large
XX CC intestine, lung, liver, prostate, pancreas, digestive tract, bladder,
XX CC mammary gland, uterus, thyroid gland and ovary. Accordingly, this
XX CC composition exhibits cytostatic activity. This polynucleotide sequence is
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FT 21567. .21762
FT /*tag= f
FT /number= 3
FT 21763. .23851
FT /*tag= g
FT /number= 3
FT 23852. .24032
FT /*tag= h
FT /number= 4
FT 24033. .24719
FT /*tag= i
FT /number= 4
FT 24720. .24899
FT /*tag= j
FT /number= 5
FT 24900. .25393
FT /*tag= k
FT /number= 5
FT 25394. .25549
FT /*tag= l
FT /number= 6
FT 25550. .30195
FT /*tag= m
FT /number= 6
FT 30196. .30292
FT /*tag= n
FT /number= 7
FT 30293. .31272
FT /*tag= o
FT /number= 7
FT 31273. .31358
FT /*tag= p
FT /number= 8
FT 31359. .33843
FT /*tag= q
FT /number= 8
FT 33844. .33957
FT /*tag= r
FT /number= 9
FT 33958. .35941
FT /*tag= s
FT /number= 9
FT 35942. .36013
FT /*tag= t
FT /number= 10
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FT 37885. .38073
FT /*tag= v
FT /number= 11
FT 38074. .41874
FT /*tag= w
FT /number= 11
FT 41875. .42001
FT /*tag= x
FT /number= 12
FT 42002. .42881
FT /*tag= y
FT /number= 12
FT 42882. .42943
FT /*tag= z
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FT 42944. .46129
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FT 46255. .47035
FT /*tag= ac
FT /number= 14
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FT exon 47036. .47173
FT /*tag= ad
FT /number= 15
FT 47174. .47709
FT /*tag= ae
FT /number= 15
FT 47710. .50544
FT /*tag= af
FT /number= 16
XX WO200188198-A1.
XX 22-NOV-2001.
XX 15-MAY-2001; 2001WO-US015774.
XX 16-MAY-2000; 2000US-00572423.
XX 07-DEC-2000; 2000US-00733294.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Gaarde WA, Freier SM, Wancewicz E;
XX WPI; 2002-075321/10.
XX P-PSDB; RAU72735.
```

New compound targeted to nucleic acid molecule encoding telomerase transcriptase (TERT), which specifically hybridizes with and inhibits expression of TERT, useful for modulating apoptosis and inhibiting cell growth.

Example 19; Page 112-138; 154pp; English.

The invention describes a compound, 8-50 nucleobases in length targeted to a nucleic acid molecule encoding human TERT (telomerase reverse transcriptase), where the compound specifically hybridizes with and inhibits the expression of TERT. A series of oligonucleotides were designed to target different regions of a central gap region consisting of nucleotides in length and composed of the human TERT RNA. These were 20 ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-MOE) nucleotides. The compounds were analyzed for their effect on human TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction (PCR). The compound is useful for inhibiting the expression of TERT in cells or tissues, for treating a human having disease or condition associated with TERT, for modulating apoptosis, for inhibiting cell growth (preferably, cancer cell growth), in antisense therapy and for diagnostics and therapeutics. This sequence encodes human telomerase reverse transcriptase (TERT) #1, and is used to create antisense oligonucleotides which modify TERT expression, described in the method of the invention

SQ Sequence 51552 BP; 10709 A; 13313 C; 15370 G; 12158 T; 0 U; 2 Other;

Query Match 99.6%; Score 395.4; DB 6; Length 51552;

Best Local Similarity 99.7%; Pred. No. 2.4e-56;

Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 CCCTCGCTGGCGTCCCTGCACCTTGGGAGCGCGAGCGCGCGCGGGGAGCGCGCG 60
Db 10877 CCCTCGCTGGCGTCCCTGCACCTTGGGAGCGCGAGCGCGCGGGGAGCGCGC 10936
Qy 61 CCAGACCCCCCGGTCCGCGCCCGAGCAGCTGCGCTGTCTGGGGCCAGCGCGGCTCCAGTG 120
Db 10937 CCAGACCCCCCGGTCCGCGCCCGAGCAGCTGCGCTGTCTGGGGCCAGCGCGGCTCCAGTG 10996
Qy 121 GATTGCGGGGACAGAGCCCGCAGACCCCGCTTCCACGTCGCGGAGGAGACTGGGGACCC 180
Db 10997 GATTGCGGGGACAGAGCCCGCAGACCCCGCTTCCACGTCGCGGAGGAGACTGGGGACCC 11056
Qy 181 GGGCACCCTCTCTCCCTTCCCTTCCAGTCCGCTTCCCTTCCGCGGACCCCGCCCG 240
Db 11057 GGGCACCCTCTCTCCCTTCCCTTCCAGTCCGCTTCCCTTCCGCGGACCCCGCCCG 11116
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QY 241 TCCCGACCCCTCCCGGGTCCCGGGCCAGCCCTCCCGGGCCCTCCAGCCCTCCCTT 300
Db 11117 TCCGACCCCTCCCGGGTCCCGGGCCAGCCCTCCCGGGCCCTCCAGCCCTCCCTT 11176
QY 301 CTTTCCCGGGCCCGCCCTCTCTCTCGCGGCGAGTTTCAGGACGCTGCTGCT 360
Db 11177 CTTTCCCGGGCCCGCCCTCTCTCTCGCGGCGAGTTTCAGGACGCTGCTGCT 11236
QY 361 GCGCAGTGGGAGCCCTGCGCCCGCGCCACCCCGCG 397
Db 11237 GCGCAGTGGGAGCCCTGCGCCCGCGCCACCCCGCG 11273

RESULT 14
AC47272
ID ACC47272 standard; DNA; 378 BP.
XX
AC ACC47272;
DT 11-AUG-2003 (first entry)
XX
DE CEA gene cis-acting sequence.
XX
KW Gene expression; promoter; cytostatic; gene therapy; antisense therapy;
KW cancer; cis-acting; CEA gene; ds.
XX
OS Unidentified.
XX
PN WO2003013555-A1.
XX
PD 20-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024741.
XX
PR 08-AUG-2001; 2001US-0310905P.
XX
PR (TEXA ) UNIV TEXAS SYSTEM.
PA
PI Fang B;
XX
WPI; 2003-256488/25.
XX
Expressing gene products in a cell type-preferential manner with a binary
or bicistronic expression system, useful for treating cancers of the
brain, head and neck, esophagus, thyroid, stomach, colon, liver,
prostate, skin and rectum.
XX
Disclosure; Page 139; 141pp; English.
XX
The invention relates to expressing gene product in a cell type-
preferential manner. The method involves providing a first expression
cassette having a cell type-preferential promoter, providing a second
expression cassette having an inducible promoter, and transferring the
first and second expression cassettes into a cell in which the cell type
-specific preferential promoter is active. The methods and compositions
of the present invention are useful for treating cancers of the brain,
head and neck, esophagus, thyroid, stomach, colon, liver, kidney,
prostate, breast, cervix, ovaries, testicles, rectum, skin and blood. The
present sequence represents a cis-acting sequence that confers expression
of the CEA gene
XX
SQ Sequence 378 BP; 35 A; 178 C; 121 G; 44 T; 0 U; 0 Other;

Query Match 94.8%; Score 376.4; DB 8; Length 378;
Best Local Similarity 99.7%; Pred. No. 6.7e-53;
Matches 377; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 CACCTGGAGCGGACGCGCGCGCGGGGAGCGCGGCCAGACCCCGGGTCCGC 78
Db 1 CACCTGGAGCGGACGCGCGCGCGGGGAGCGCGGCCAGACCCCGGGTCCGC 60
QY 79 CCGGAGCAGCTGCTGTCTCGGGGCGAGCGCGGGCTCCAGTGGATTCTCGGCGCACAGACG 138
```

```
Db 61 CCGGAGCAGCTGCTGTCTCGGGGCGAGCCCGGGTCCAGTGGATTCTCGGCGCACAGACG 120
QY 139 CCCAGGACCGGCTTCCACAGCTGGGAGGACTGGGACCCCGGACACCCGTCCTTGCCTT 198
Db 121 CCCAGGACCGGCTTCCACAGCTGGGAGGACTGGGACCCCGGACACCCGTCCTTGCCTT 180
QY 199 TTACCTTTCAGCTCCGCTCTCTCGGCGGAGACCCCGCCCGTCCGACACCTTCCGGGT 258
Db 181 TTACCTTTCAGCTCCGCTCTCTCGGCGGAGACCCCGCCCGTCCGACACCTTCCGGGT 240
QY 259 CCGGCGCCAGCCCTCCGCGGCGCTCCAGCCCTCCCTTCTTCCGGGCGCCCGCC 318
Db 241 CCGGCGCCAGCCCTCCGCGGCGCTCCAGCCCTCCCTTCTTCCGGGCGCCCGCC 300
QY 319 CTCTCTCTCGGCGCGAGTTTCAGGACGCTGCTGCTGCTGCGCACGTTGGAGAGCCCT 378
Db 301 CTCTCTCTCGGCGCGAGTTTCAGGACGCTGCTGCTGCTGCGCACGTTGGAGAGCCCT 360
QY 379 GCGCGCGCGCACCCCGCG 396
Db 361 GCGCGCGCGCACCCCGCG 378

RESULT 14
AAD27972/c
ID AAD27972 standard; DNA; 35871 BP.
XX
AC AAD27972;
DT 16-JUL-2002 (first entry)
XX
DE Recombinant adenovirus vector KD3-TERT.
XX
KW Recombinant adenovirus vector; adenovirus death protein; ADP; telomerase;
KW human; telomerase reverse transcriptase promoter; TERT; neoplastic cell;
KW cancer; KD3-TERT; E1A region; mutant; ds.
XX
OS Mastadenovirus.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
PN US2002028785-A1.
XX
PD 07-MAR-2002.
XX
PF 19-SEP-2001; 2001US-00956335.
XX
PR 12-JUL-1999; 99US-00351778.
XX
PR 20-SEP-2000; 2000US-0233872P.
XX
PA (UYSL-) UNIV SAINT LOUIS.
XX
PI Wold WSM, Toth K, Tollefson AE, Kuppaswamy M;
XX
WPI; 2002-328910/36.
XX
Novel recombinant adenovirus vector useful for destroying neoplastic
PT cells, comprises a human telomerase reverse transcriptase promoter and at
PT least one inactivation mutation in the E3 region.
XX
Claim 5; Page 28-44; 64pp; English.
XX
The invention relates to a recombinant adenovirus vector which
overexpresses an adenovirus death protein (ADP) and which is replication-
restricted to cells expressing telomerase, comprises a human telomerase
reverse transcriptase promoter (hTERT) and at least one inactivating
mutation in the E3 region. The vector of the invention is useful in vitro
for promoting death of a cell expressing telomerase, and for promoting
death of neoplastic cells in a patient. The adenovirus vector is an
efficient and effective anticancer agent that could specifically target
neoplastic cells, while replicating poorly or not at all in normal
```


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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 05:56:54 ; Search time 1998.54 Seconds
(without alignments)
4666.271 Million cell updates/sec

Title: US-10-081-969-94

Perfect score: 245

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Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	77.2	31.5	1285	9 AG334095	AG334095 Mus muscu
C 2	75.8	30.9	1695	8 CC290874	CC290874 CH261-172
C 3	75.4	30.8	941	9 CL465224	CL465224 SAIL_1236
C 4	75	30.6	566	9 CNG03JNO	AL247077 Tetradon
C 5	74.4	30.4	881	5 BX427015	BX427015 BX427015
C 6	74.4	30.4	969	9 CL477043	CL477043 SAIL_267
C 7	74.4	30.4	988	9 CL477397	CL477397 SAIL_272
C 8	73.8	30.1	468	5 BQ608819	BQ608819 BRY_4732
C 9	73.6	30.0	794	8 BZ050856	BZ050856 jnr64f12
C 10	73.6	30.0	1233	9 AG341388	AG341388 Mus muscu
C 11	73.4	30.0	949	9 CL465953	CL465953 SAIL_1249
C 12	73.4	30.0	1270	9 AG382572	AG382572 Mus muscu
C 13	73.2	29.9	1081	9 CL464716	CL464716 SAIL_1225
C 14	72.8	29.7	759	9 AG126157	AG126157 Pan trogl
C 15	72.6	29.6	675	8 BZ050815	BZ050815 jnr64a12
C 16	72.6	29.6	897	9 CL459907	CL459907 SAIL_104
C 17	72.4	29.6	1400	9 AG429585	AG429585 Mus muscu
C 18	72.4	29.6	1531	9 AG430426	AG430426 Mus muscu
C 19	72.2	29.5	1197	4 BI416470	BI416470 hasp001xa
C 20	72.2	29.5	1449	9 AG360973	AG360973 Mus muscu
C 21	72	29.4	1008	9 AG395157	AG395157 Mus muscu
C 22	71.8	29.3	1289	9 CL447104	CL447104 ISB1-1568
C 23	71.6	29.2	458	9 CNG0002T	AL060559 Drosophil
C 24	71.6	29.2	944	9 AG062271	AG062271 Pan trogl

25	71.6	29.2	963	9	CL475743	CL475743 SAIL_242b
26	71.6	29.2	1026	5	BU900073	BU900073 AGENCOURT
27	71.4	29.1	795	8	AZ188474	AZ188474 SP_1012_A
C 28	71.4	29.1	926	9	AG061568	AG061568 Pan trogl
C 29	71.4	29.1	1285	5	BU168242	BU168242 AGENCOURT
C 30	71.4	29.1	1523	9	AG448267	AG448267 Mus muscu
C 31	71.4	29.1	1713	9	AG435689	AG435689 Mus muscu
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33	71	29.0	1101	9	CNS0153F	AL104949 Drosophil
34	70.8	28.9	909	9	CL483192	CL483192 SAIL_378
35	70.8	28.9	928	9	CL478793	CL478793 SAIL_297
36	70.8	28.9	952	5	BU557852	BU557852 AGENCOURT
C 37	70.8	28.9	1066	6	CB905393	CB905393 trico074xd
C 38	70.8	28.9	1066	7	CF876920	CF876920 trico074xd
39	70.6	28.8	705	8	BZ051861	BZ051861 jnr57a10
C 40	70.6	28.8	781	2	BF865678	BF865678 963061E04
C 41	70.6	28.8	855	1	AL573255	AL573255 AL573255
42	70.6	28.8	1077	9	CL493953	CL493953 SAIL_589
43	70.6	28.8	1109	9	CL515456	CL515456 SAIL_8_E1
44	70.6	28.8	1328	9	AG320910	AG320910 Mus muscu
C 45	70.6	28.8	1675	9	AG360980	AG360980 Mus muscu

ALIGNMENTS

RESULT 1
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LOCUS AG334095 1285 bp DNA linear GSS 02-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-124N12.TJ, genomic survey
sequence.
ACCESSION AG334095
VERSION AG334095.1 GI:47907405
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
2 (bases 1 to 1285)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@sc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@tc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@tc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY Vector : pBac3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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Best Local Similarity 58.0%; Pred. No. 7e-05;
Matches 127; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 26 CCGGGACACCGGTCCTTCCAGCTCCGCTCTCTCCGCGCGGACCCCGCC 85
DB 845 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 786

QY 86 CCGTCCCGACCCCTCCCGGGTCCCGGCGAGCCCTCTCCGCGCGCTCCCGCCCTCC 145
DB 785 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 726

QY 146 CTTCTTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 205
DB 725 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 666

QY 206 GCTGCGCAGCTGGGAAGCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 244
DB 665 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 627

RESULT 2
LOCUS CC290874 1695 bp DNA linear GSS 13-MAY-2003
DEFINITION CH261-172N5_Sp6.1 CH261 Gallus gallus genomic clone CH261-172N5,
ACCESSION CC290874
VERSION CC290874.1 GI:30662315
KEYWORDS GSS.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE 1 (bases 1 to 1695)
AUTHORS Warren, W., Graves, T., Mardis, E. and Wilson, R.
TITLE Gallus gallus BAC End Reads
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTAGTGACACTATAG
Class: BAC ends
High quality sequence start: 26
High quality sequence stop: 136.
FEATURES
Location/Qualifiers
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/cell_line="UCD001, inbred 256"
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ORIGIN
Query Match          30.9%; Score 75.8; DB 8; Length 1695;
Best Local Similarity 57.3%; Pred. No. 0.00012;
Matches 125; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 26 CCGGGACACCGGTCCTTCCAGCTCCGCTCTCTCCGCGCGGACCCCGCC 85
DB 1420 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1479

us-10-081-969-94.rst
QY 86 CCGTCCCGACCCCTCCCGGGTCCCGGCGCGCGCGCGCGCGCGCGCGCGCTCC 145
DB 1480 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1539

QY 146 CTTCTTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 205
DB 1540 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1599

QY 206 GCTGCGCAGCTGGGAAGCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 243
DB 1600 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1637

RESULT 3
LOCUS SAIL_1236_D06.v1 941 bp DNA linear GSS 31-MAR-2004
DEFINITION SAIL_1236_D06.v1, genomic survey sequence.
ACCESSION CL465224
VERSION CL465224.1 GI:45868129
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 941)
AUTHORS Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D., Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J. D., Cotton, D., Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B., Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S. A.
TITLE A high-throughput Arabidopsis reverse genetics system
JOURNAL Plant Cell 14 (12), 2985-2994 (2002)
MEDLINE 22356987
PUBMED 12468722
COMMENT Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwalis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS845346; T-DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not single contiguous sequences.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
1..941
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone_lib="SAIL Collection"
/clone="SAIL 1236_D06.v1"
/notes="T-DNA left border sequences were isolated using a modified TAIL-PCR strategy"

ORIGIN
Query Match          30.8%; Score 75.4; DB 9; Length 941;
Best Local Similarity 56.9%; Pred. No. 0.00016;
Matches 136; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 7 GTGGCGGAGGACGTGGGGACCCGGGACCCGCTTCGCGCGCTTCACCTTCAGCTCCGCT 66
DB 608 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667

QY 67 CTTCCGCGGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 126
DB 668 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727

QY 127 GGCCTTCCAGCGCGCTTCCTTTCGCGCGCGCGCGCGCGCGCGCGCGCG 186
DB 728 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 787
```


LOCUS CL477043 969 bp DNA linear GSS 01-APR-2004
DEFINITION SAIL_267_A03.v1 SAIL Collection Arabidopsis thaliana genomic clone
SAIL_267_A03.v1, genomic survey sequence.
ACCESSION CL477043
VERSION CL477043.1 GI:45943329
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 969)
AUTHORS Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
TITLE A high-throughput Arabidopsis reverse genetics system
JOURNAL Plant Cell 14 (12), 2985-2994 (2002)
MEDLINE 22356987
PUBMED 12468722
COMMENT Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS812359; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1..969
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone_lib="SAIL_267_A03.v1"
/clone="SAIL_267_A03.v1"
/note="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"
ORIGIN
Query Match 30.4%; Score 74.4; DB 9; Length 969;
Best Local Similarity 57.5%; Pred. No. 0.00024;
Matches 126; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 26 CCGGGCACCCGTCCTGCCCCCTTACCTTCCAGCTCCGCTCTCCGGCGGAGACCCGCG 85
DB 531 CCCCCCCCCCNCNCC 590
QY 86 CCGTCCGACCCCTCCCGGTCCCGGCCAGCCCCCTCCGGGCCCTCCAGCCCTCC 145
DB 591 CC 650
QY 146 CTTCTTTCGGCGCCCGCCCTCTCTCTCCGCGCGGAGTTTCAGGCAGCGTGCCT 205
DB 651 CC 710
QY 206 GCTGCGACGTGGGAAGCCCTTGGCCCGCGGACCCCGCC 244
DB 711 GCGGGGGGGGCG 749
RESULT 7
CL477397 988 bp DNA linear GSS 01-APR-2004
LOCUS SAIL_272_B09.v1 SAIL Collection Arabidopsis thaliana genomic clone
DEFINITION SAIL_272_B09.v1, genomic survey sequence.
ACCESSION CL477397
VERSION CL477397.1 GI:45944169
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 988)
AUTHORS Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
TITLE A high-throughput Arabidopsis reverse genetics system
JOURNAL Plant Cell 14 (12), 2985-2994 (2002)
MEDLINE 22356987
PUBMED 12468722
COMMENT Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS812603; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1..988
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone_lib="SAIL_272_B09.v1"
/clone="SAIL_272_B09.v1"
/note="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"
ORIGIN
Query Match 30.4%; Score 74.4; DB 9; Length 988;
Best Local Similarity 56.3%; Pred. No. 0.00024;
Matches 138; Conservative 0; Mismatches 107; Indels 0; Gaps 0;
QY 1 CCCCACGTGGGGAGGACTGGGGACCGGGGACCCGTCCTGCTCCCTTCCAGCTTCCAGCT 60
DB 429 CC 488
QY 61 CCGCTCTCTCCGCGGAGACCCCGCCCGTCCGACCCCTCCCGGTCCTCCGCGGCGCC 120
DB 489 CCGCGCGCCCGCC 548
QY 121 CTTCCGGGCTCCAGCCCTTCCCTTCTTTCGGGCGCCCGCCCTCTCTCTCGGGCG 180
DB 549 CCCCCCGCGCGCCCGCG 608
QY 181 CGAGTTTTCAGGCAGCGCTCGTCTCTGCGCACGTGGGAAGCCTTGGGCCCGCCACC 240
DB 609 GCGGGGGGGCG 668
QY 241 CCGCG 245
DB 669 CCGCG 673
RESULT 8
BQ608819/c 468 bp mRNA linear EST 25-JUN-2002
LOCUS BRY_4732 wheat EST endosperm library Triticum aestivum cDNA 5',
DEFINITION mRNA sequence.
ACCESSION BQ608819
VERSION BQ608819.1 GI:21558158
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 468)
AUTHORS Clarke,B., Lambrecht,M. and Rhee,S.Y.
TITLE Arabidopsis genomic information for interpreting wheat EST sequences
JOURNAL Punct. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE 22478026
PUBMED 12590341
COMMENT Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhee@acoma.stanford.edu.

FEATURES

source

1..468
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mrna"
/cultivar="Wyuna"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA (days post anthesis)"
/clone_lib="wheat EST endosperm library"

ORIGIN

Query Match 30.1%; Score 73.8; DB 5; Length 468;
Best Local Similarity 57.5%; Pred. No. 0.00033;
Matches 126; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 26 CCGCGCACCTCTCGCCCTTCACTTCAGCTCCGCTCTCCGCGGACCCCGCC 85
DB 396 CCGCGCCGCCCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCG 337
QY 86 CGTCCGACCTCTCCGGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 145
DB 336 GCGCCG 277
QY 146 CTTCTTTTCGCGGCGCGCGCGCGCTCTCTCGCGCGCGAGTTTCAGCGAGCTGCT 205
DB 276 CCG 217
QY 205 GTGCGCACGTGGGAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 244
DB 216 CCG 178

RESULT 9

BZ050856

LOCUS

DEFINITION jnr54f12.b1 B.oleracea001 Brassica oleracea genomic, genomic survey sequence.

ACCESSION

BZ050856

VERSION

BZ050856.1

KEYWORDS

GSS.

SOURCE

Brassica oleracea

ORGANISM

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 794)

AUTHORS

Delehaunty,K., Fellw,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.

TITLE Whole genome shotgun reads from Brassica oleracea

JOURNAL Unpublished (2002)

COMMENT Contact: Richard K. Wilson

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Plate: jnr54 row: f column: 12

Seq primer: -2UpPOT forward

Class: shotgun

FEATURES

source

High quality sequence start: 137
High quality sequence stop: 551.
Location/Qualifiers
1..794
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea001"
/note="vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN

Query Match 30.0%; Score 73.6; DB 8; Length 794;
Best Local Similarity 53.3%; Pred. No. 0.00034;
Matches 130; Conservative 0; Mismatches 114; Indels 0; Gaps 0;
QY 1 CCCCACGTGGCGGAGCTGGGACCGCGGACCGCTCTGCCCCCTTCACCTTCAGCT 60
DB 291 CCCCCCGGG 350
QY 61 CCGGCTCTCTCGCGGAGACCGCGGCGGCTCTCGGAGACCTCTCGGGTCTCCGCGCCAGCCC 120
DB 351 CCCCCCGGG 410
QY 121 CTTCCGGGCTTCCAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 411 CCCCCCGGG 470
QY 181 CGAGTTTCAGCGAGCGCTGCGTCTGTCGCGACGTCGAGAGCCCTGCGCGCCGCGCCACCC 240
DB 471 CCCCCCGGG 530
QY 241 CCGC 244
DB 531 CCGC 534

RESULT 10

AG341388

LOCUS

DEFINITION Mus musculus molossinus DNA, clone:MSMg01-134L24.T7, genomic survey sequence.

ACCESSION

AG341388

VERSION

AG341388.1

KEYWORDS

GSS.

SOURCE

Mus musculus molossinus

ORGANISM

Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

TITLE BAC end Sequences of Library MSMg01

JOURNAL Unpublished

2 (bases 1 to 1233)

AUTHORS

Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

TITLE Direct Submission

JOURNAL

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehito-chou,Tsaurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@ipc.riken.jp URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@ipc.riken.jp).

Tsukuba Institute, Bio Resource Center,

The Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199

e-mail: abe@ipc.riken.jp


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/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-193C09.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match      30.0%; Score 73.4; DB 9; Length 1270;
Best Local Similarity 56.1%; Pred. No. 0.00036;
Matches 137; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 1 CCCACGTGGCGGAGGACTGGGACCCGGGACACCGCTCTGCTCCCTTCACCTTCACGT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 864 CCCCCCGCGGCCCCCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 923

QY 61 CGGCTCTCCGCGGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 924 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 983

QY 121 CCTCGGGCCCTCCAGGCCCTCCCTCTTCTTCGCGCGCGCGCGCGCGCGCGCGCGCG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 984 CGGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 1043

QY 181 CGAGTTTACGGCAGCGCTGCTGCTGCTGCGCACGTGGAGACCTTGCGCGCGCGCACCC 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1044 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 1103

QY 241 CGCG 244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1104 CCCC 1107

RESULT 13
CL464716
LOCUS      CL464716          1081 bp      DNA      linear      GSS 31-MAR-2004
DEFINITION SAIL_1225_G10.v1 SAIL Collection Arabidopsis thaliana genomic clone
ACCESSION  CL464716
VERSION     CL464716.1 GI:45867621
KEYWORDS   GSS
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1 (bases 1 to 1081)
AUTHORS   Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
            Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
            Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
            Mittel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
            A high-throughput Arabidopsis reverse genetics system
            Plant Cell 14 (12), 2985-2994 (2002)
JOURNAL   MEDLINE
PUBMED   22356987
COMMENT   Contact: Sessions A
            Applied Trait Genetics
            Syngenta Biotechnology Inc.
            3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
            Email: allen.sessions@syngenta.com
            ABRC Stock Number CS944896; T-DNA left border flanking sequences of
            Syngenta Arabidopsis Insertion Library (SAIL) lines are available
            through the Arabidopsis Biological Resource Center (ABRC).
            Sequences represent a pool of amplified genomic regions and not
            single contiguous sequences.
            Class: TDNA tagged.
            Location/Qualifiers
                1..1081
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /ecotype="Columbia"
                /db_xref="taxon:3702"
                /clone="SAIL_1225_G10.v1"

FEATURES
source
    1..1081
        /organism="Arabidopsis thaliana"
        /mol_type="genomic DNA"
        /db_xref="taxon:3702"
        /clone="SAIL_1225_G10.v1"

/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-193C09.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match      29.9%; Score 73.2; DB 9; Length 1081;
Best Local Similarity 56.5%; Pred. No. 0.0004;
Matches 135; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 7 GTGGCGGAGGACTGGGACCCGGGACCCCGCTCTGCTCCCTTCACCTTCACGTCCGCT 66
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 387 GGGGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 446

QY 67 CTTGCGCGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 447 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 506

QY 127 GGCCCTCCAGCCCTCCCTTCTTCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 507 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 566

QY 187 TCAGCGACGCTGCTGCTGCTGCGCACGTGGAGACCTTGCGCGCGCGCGCGCGCGCG 245
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 567 CCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 625

RESULT 14
AG126157/c
LOCUS      AG126157          759 bp      DNA      linear      GSS 04-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-136K03.F, genomic survey sequence.
ACCESSION  AG126157
VERSION     AG126157.1 GI:16655322
KEYWORDS   GSS.
SOURCE     Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE  1
AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
            BAC end sequences of Library PTB
            Unpublished
            2 (bases 1 to 759)
            Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
            Direct Submission
            Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsuri-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimbeg@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
            Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
            PRIMERS
            Sequencing: -21M13
            LIBRARY
            Vector      : pKS145
            R.Site 1    : SacI
            R.Site 2    : SacI
            Location/Qualifiers
                1..759
                /organism="Pan troglodytes"
                /mol_type="genomic DNA"
                /db_xref="taxon:9598"
                /clone="PTB-136K03.F"
                /sex="male"
                /cell_type="lymphoblast"
                /clone_lib="PTB Chimpanzee Male BAC Library"

Query Match      29.7%; Score 72.8; DB 9; Length 759;
Best Local Similarity 55.7%; Pred. No. 0.00049;
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	Matches	122;	Conservative	0;	Mismatches	97;	Indels	0;	Gaps	0;
Qy	26	CCCGGACACCGTCTCTGCCCTTACCTTCAGTTCGCGCTCTCTCGGGGAGACCCGCC	85							
Db	551	CC	492							
Qy	86	CGTCCCGACCCCTCCGGGTCCCGGGCCAGCCCTCCGGGGCCCTCCAGAGCCCTCCC	145							
Db	491	CC	432							
Qy	146	CTTCTTTTCCGGGCGCCCGCCCTCTCTCGGGGCGAGTTCTCAGGACGCGTCGTCCT	205							
Db	431	CNNCC	372							
Qy	206	GCTCGCACGTGGGAGCCCTGGGCCCGGGCCACCCCGGC	244							
Db	371	CNNNNCCCGGGGCAACCCCCCCCCCNCNCNCNCCCCCCCC	333							

RESULT 15
BZ050815
LOCUS
DEFINITION
BZ050815
jnr64a12.b1 B.oleracea001 Brassica oleracea genomic, genomic survey
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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FEATURES
source
    high quality sequence shotp: 333.
    Location/Qualifiers
        1. .675
            /organism="Brassica oleracea"
            /mol_type="genomic DNA"
            /db_xref="taxon:3712"
            /clone_lib="B.oleracea001"
            /note="Vector: pOW13; Whole genome shotgun library from
            flowering buds. DNA was purified from a crude nuclear
            prep using Brassica oleracea T01000H3 buds provided by
            Thomas Osborn at the University of Wisconsin. Genomic
            DNA was provided by Pablo Rabinowicz (CSHL) and the
            shotgun library prepared at Washington University Genome
            Sequencing Center."

```

	Query Match	29.6%	Score 72.6	DB 8	Length 675
	Best Local Similarity	56.8%	Pred. No. 0.00054		
	Matches 129	Conservative 0	Mismatches 98	Indels 0	Gaps 0
Qy	19	CTGGGGACCCGGGACCCGCTCTGCCCTTCACCTTCAGTCCGCTCTCCCGGGGA	78		
Db	204	CCGGCCCCCNC	263		
Qy	79	CCCCGCCCCCTCCGAGCCCTTCGCGGGTCCCGGGCCAGCCCCCTCGGGGCCCTCCAGC	138		
Db	264	CCCCCCCCCCCCCCCCCCCCCGCGCTTCCCCCCCCCCCCCCCCCCCCCCCCCTGTC	323		

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Qy 139 CCCTCCCTTCTTTCGGGGCGGGCCCTCTCTCGGGGGCGAGTTTCAGGCAGCGT 198
Db 324 CCCCCCTCTCCCTCCCGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCT 383

Qy 199 GCGTCTGTCTCGCAGTGGGAAGCCCTGGCGCCCGGCCACCCCCGG 245
Db 384 CCCCCCGCCCCCGCCCCCGCCCCCGCCCGCCCTCCCCCGCCCCCG 430

Search completed: April 9, 2005, 10:27:49
Job time : 2005.54 secs

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Search completed: April 9, 2005, 10:27:49
Job time : 2005.54 secs

	Query Match	100.0%	Score 397	DB 6	Length 397
	Best Local Similarity	100.0%	Pred. No. 8.2e-49		
	Matches 397	Conservative 0	Mismatches 0	Indels 0	Gaps 0
1	CCCTCGCTGGCGTCCCTGCACCTCGGAGCGCGAGCGCGCGCGGGGAGCGCGC	60			
Db	1	CCCTCGCTGGCGTCCCTGCACCTCGGAGCGCGAGCGCGCGGGGAGCGCGC	60		
61	CCAGACCCCCGGGTCCGCCGGAGCAGCTGCTGCGGGGCCAGGCCGGGCTCCCAATG	120			
Db	61	CCAGACCCCCGGGTCCGCCGGAGCAGCTGCTGCGGGGCCAGGCCGGGCTCCCAATG	120		
121	GATTGCGGGGACACAGACGCCACGAGCCGGGCTTCCACGTGCGGAGGGAAGCTGGGACCC	180			
Db	121	GATTGCGGGGACACAGACGCCACGAGCCGGGCTTCCACGTGCGGAGGGAAGCTGGGACCC	180		
181	GGGACACCGGTCTCTGCGCCCTTACCTTCCAGCTCCCGCTCCTCGCGCGGACCCCGCCCGG	240			

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Db      181  GGGCACCCTGCTGCCCCCTTACCTTCCAGCTCCGCTCTCTCCGCGCGAGACCCCGCCCG 240
Qy      241  TCCGAGACCTCCCGGTTCCCGGCCAGCCCTTCCGGGCCCTCCAGCCCTCCCTT 300
Db      241  TCCGAGACCTCCCGGTTCCCGGCCAGCCCTTCCGGGCCCTCCAGCCCTCCCTT 300
Qy      301  CTTTTCCGGGGCCCGCCCTCTCTCTCGCGCGGAGTTTCAGGCAGCGCTGCTGCT 360
Db      301  CTTTTCCGGGGCCCGCCCTCTCTCTCGCGCGGAGTTTCAGGCAGCGCTGCTGCT 360
Qy      361  GCGCAGCTGGGAGCCCTCGCCCGCGCCACCCCGCG 397
Db      361  GCGCAGCTGGGAGCCCTCGCCCGCGCCACCCCGCG 397

RESULT 2
AF098956      2043 bp      DNA      linear      PRI 05-FEB-1999
LOCUS      Homo sapiens telomerase reverse transcriptase (TERT) gene, promoter
DEFINITION      region and partial cds.
ACCESSION      AF098956
VERSION      AF098956.1 GI:4226057
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      1 (bases 1 to 2043)
JOURNAL      Horikawa,I., Cable,P.L., Afshari,C. and Barrett,J.C.
MEDLINE      Cloning and characterization of the promoter region of human
PUBMED      telomerase reverse transcriptase gene
          Cancer Res. 59 (4), 826-830 (1999)
          99151529
          10029071
REFERENCE      2 (bases 1 to 2043)
AUTHORS      Horikawa,I., Cable,P.L., Afshari,C. and Barrett,J.C.
TITLE      Direct Submission
JOURNAL      Submitted (15-OCT-1998) Laboratory of Molecular Carcinogenesis,
          National Institute of Environmental Health Sciences, 111 T. W.
          Alexander Drive, P.O. Box 12233, Research Triangle Park, NC 27709,
          USA
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             /chromosome="5"
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             1..1665
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             /product="telomerase reverse transcriptase"
             /protein_id="AA012786.1"
             /db_xref="GI:4226059"
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ORIGIN
Query Match      100.0%; Score 397; DB 9; Length 2043;
Best Local Similarity      100.0%; Pred. No. 4.6e-49;
Matches 397; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1      CCCTCGCTGGCGTCCCTGCACTTGGGAGCGCGAGCGCGCGGGGGGGAAGCGCGG 60
Db      1324  CCCTCGCTGGCGTCCCTGCACTTGGGAGCGCGAGCGCGCGGGGGGGAAGCGCGG 1383
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Qy      61      CCAGACCCCGGGTCCGCCCGAGCAGCTGCGCTGTTCGGGGCCAGGCGGGCTCCCAATG 120
Db      1384  CCAGACCCCGGGTCCGCCCGAGCAGCTGCGCTGTTCGGGGCCAGGCGGGCTCCCAATG 1443
Qy      121  GATTTCGGGGGACAGAGCCCGCAGACCGCGCTTCCACGTGCGGAGGAGACTGGGGACCC 180
Db      1444  GATTTCGGGGGACAGAGCCCGCAGACCGCGCTTCCACGTGCGGAGGAGACTGGGGACCC 1503
Qy      181  GGGCACCCTGCTCGCCCTTCCAGCTTCGCGCTTCCTCCGCGCGGACCCCGCCCG 240
Db      1504  GGGCACCCTGCTCGCCCTTCCAGCTTCGCGCTTCCTCCGCGCGGACCCCGCCCG 1563
Qy      241  TCCGACCCCTTCCGGGTTCGCCGCCAGCCCTTCCGCGGCCCTCCAGCCCTCCCTT 300
Db      1564  TCCGACCCCTTCCGGGTTCGCCGCCAGCCCTTCCGCGGCCCTCCAGCCCTCCCTT 1623
Qy      301  CTTTTCCGGGGCCCGCCCTCTCTCGCGGGCGGAGTTTCAGGCAGCGCTGCTGCT 360
Db      1624  CTTTTCCGGGGCCCGCCCTCTCTCTCGCGGGCGGAGTTTCAGGCAGCGCTGCTGCT 1683
Qy      361  GCGCAGCTGGGAGCCCTGCGCCCGCGCCACCCCGCG 397
Db      1684  GCGCAGCTGGGAGCCCTGCGCCCGCGCCACCCCGCG 1720

RESULT 3
AR390473      4321 bp      DNA      linear      PAT 18-DEC-2003
LOCUS      Sequence 6 from patent US 6610839.
DEFINITION      AR390473
ACCESSION      AR390473
VERSION      AR390473.1 GI:40112397
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 4321)
AUTHORS      Morin,G.B. and Andrews,W.H.
TITLE      Promoter for telomerase reverse transcriptase
JOURNAL      Patent: US 6610839-A 6 26-AUG-2003;
FEATURES      Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 397; DB 6; Length 4321;
Best Local Similarity      100.0%; Pred. No. 3.6e-49;
Matches 397; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1      CCCTCGCTGGCGTCCCTGCACTTGGGAGCGCGAGCGCGGGGGGGAAGCGCGG 60
Db      2086  CCCTCGCTGGCGTCCCTGCACTTGGGAGCGCGAGCGCGGGGGGGAAGCGCGG 2145
Qy      61      CCAGACCCCGGGTCCGCCCGAGCAGCTGCGCTGTTCGGGGCCAGGCGGGCTCCCAATG 120
Db      2146  CCAGACCCCGGGTCCGCCCGAGGAGCTGCGCTGTTCGGGGCCAGGCGGGCTCCCAATG 2205
Qy      121  GATTTCGGGGGACAGAGCCCGCAGACCGCGCTTCCACGTGCGGAGGAGACTGGGGACCC 180
Db      2206  GATTTCGGGGGACAGAGCCCGCAGACCGCGCTTCCACGTGCGGAGGAGACTGGGGACCC 2265
Qy      181  GGGCACCCTGCTCGCCCTTCCAGCTTCGCGCTTCCTCCGCGCGGACCCCGCCCG 240
Db      2266  GGGCACCCTGCTCGCCCTTCCAGCTTCGCGCTTCCTCCGCGCGGACCCCGCCCG 2325
Qy      241  TCCGACCCCTTCCGGGTTCGCCGCCAGCCCTTCCGCGGCCCTCCAGCCCTCCCTT 300
Db      2326  TCCGACCCCTTCCGGGTTCGCCGCCAGCCCTTCCGCGGCCCTCCAGCCCTCCCTT 2385
Qy      301  CTTTTCCGGGGCCCGCCCTCTCTCTCGCGGGCGGAGTTTCAGGCAGCGCTGCTGCT 360
Db      2386  CTTTTCCGGGGCCCGCCCTCTCTCTCGCGGGCGGAGTTTCAGGCAGCGCTGCTGCT 2445
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Qy 361 GCGCAGTGGGAAGCCCTGGCCCCCGGCCACCCCGCG 397
Db 2446 GCGCAGTGGGAAGCCCTGGCCCCCGGCCACCCCGCG 2482

RESULT 4
AF097365 4356 bp DNA linear PRI 02-FEB-1999
LOCUS Homo sapiens telomerase reverse transcriptase (TERT) gene, promoter
and partial cds.
ACCESSION AF097365
VERSION AF097365.1 GI:4210970
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4356)
AUTHORS Cong, Y.S., Wen, J. and Bacchetti, S.
TITLE The human telomerase catalytic subunit hTERT: organization of the
gene and characterization of the promoter
JOURNAL Hum. Mol. Genet. 8 (1), 137-142 (1999)
MEDLINE 99105927
PUBMED 9887342
REFERENCE 2 (bases 1 to 4356)
AUTHORS Cong, Y.S., Wen, J. and Bacchetti, S.
TITLE Direct Submission
JOURNAL Submitted (05-OCT-1998) Pathology, McMaster University, 1200 Main
St. W., Hamilton, ON L8N 3Z5, Canada
FEATURES
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        3600 CCCTCGCTGGGTCCCTGACCCCTGGAGCGAGCGCGCGCGCGGAGCGCGG 3659
        61 CCAGACCCCGGGTCCGCGCGGAGCAGCTGGCGCTGTGCGGGCGCAGCGCGGCTCCCA 120
        3660 CCAGACCCCGGGTCCGCGCGGAGCAGCTGGCGCTGTGCGGGCGCAGCGCGGCTCCCA 3719
        121 GATTGCGGGGCACAGACCGCCAGGACCGCGCTTCCACGTGCGGAGGAGCTGGGGACCC 180
        3720 GATTGCGGGGCACAGACCGCCAGGACCGCGCTTCCACGTGCGGAGGAGCTGGGGACCC 3779
        181 GGGACCCGCTCTGCGCCCTTACCTTCAGCTCCGCTCCCTCCGCGGAGCCCGCGCCCG 240
        3780 GGGACCCGCTCTGCGCCCTTACCTTCAGCTCCGCTCCCTCCGCGGAGCCCGCGCCCG 3839

Qy 241 TCCGACCCCTCCCGGTCCCGGCGCCAGCCCTCCGCGCCCTCCAGACCCCTCCCTT 300
Db 3840 TCCGACCCCTCCCGGTCCCGGCGCCAGCCCTCCGCGCCCTCCAGACCCCTCCCTT 3899

Qy 301 CTTTTCGCGCGCGCCCTCTCTCTCGCGCGGAGTTTTCAGGCGAGCGCTCGTCTCTCT 360
Db 3900 CTTTTCGCGCGCGCCCTCTCTCTCGCGCGGAGTTTTCAGGCGAGCGCTCGTCTCTCT 3959

Qy 361 GCGCAGTGGGAAGCCCTGGCCCCCGGCCACCCCGCG 397
Db 3960 GCGCAGTGGGAAGCCCTGGCCCCCGGCCACCCCGCG 3996

RESULT 5
AF121948 15332 bp DNA linear PRI 11-APR-1999
LOCUS Homo sapiens telomerase reverse transcriptase (TERT) gene, partial
cds.
ACCESSION AF121948
VERSION AF121948.1 GI:4580662
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 15332)
AUTHORS Greenberg, R.A., O'Hagan, R.C., Deng, H., Xiao, Q., Hann, S.R.,
Adams, R.R., Lichtsteiner, S., Chin, L., Morin, G.B. and DePinho, R.A.
TITLE Telomerase reverse transcriptase gene is a direct target of c-Myc
but is not functionally equivalent in cellular transformation
JOURNAL Oncogene 18 (5), 1219-1226 (1999)
MEDLINE 99144726
PUBMED 10022128
REFERENCE 2 (bases 1 to 15332)
AUTHORS Morin, G.B., Carlos, R. and Adams, R.R.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-1999) Geron Corporation, 230 Constitution Drive,
Menlo Park, CA 94025, USA
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            LVAPSCAYQVCTPPLYQLGATQAPPPHAGSGPRRLGCCRANWHSVREAGVPLGLPA
            PGARRGGSASRLPLKPRRRGAAPPERTPVCGGSAHPGTRGTGSDRGFCVVSPA
            RPAEATSLGALSSTRSHSPVGRHHAGPPSTRPPRWDTPCPVYAEIKHFLYS
            SGDKELRPSFLSLRSLTARRLVETIFLGRPPMPGTFRLLPRLPQRYWQMRPL
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        Best Local Similarity 100.0%; Pred. No. 2,3e-49;
        Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTCGCTGGGTCCCTGACCCCTGGAGCGAGCGCGCGCGGAGCGCGG 60
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Db 13105 CCTTGGCTGGCTCCTTGACCTTGGAGCGCGAGCGCGCGGGAGCGCGC 13164
Qy 61 CCAGACCCCGGGTCCGCGGAGAGCTGCGCTGTGCGGGGCGAGCGCGGGTCCAGTG 120
Db 13165 CCAGACCCCGGGTCCGCGGAGAGCTGCGCTGTGCGGGGCGAGCGCGGGTCCAGTG 13224
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Db 13225 GATTGCGGGGACAGAGCGCCAGGACCGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 13284
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Qy 301 CTTTCCGGGCGCCCGCTCTCTCCGCGGCGAGTTTTCAGGACGCTGCTGCT 360
Db 13405 CTTTCCGGGCGCCCGCTCTCTCCGCGGCGAGTTTTCAGGACGCTGCTGCTGCT 13464
Qy 361 GCGCAGCTGGGAGCGCTGCGCCCGGCGACCCCGCG 397
Db 13465 GCGCAGCTGGGAGCGCTGCGCCCGGCGACCCCGCG 13501

RESULT 6
AR342806
LOCUS AR342806 15418 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6576464.
ACCESSION AR342806
VERSION AR342806.1 GI:33738009
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Gold,J.D. and Lebkowski,J.S.
TITLE Methods for providing differentiated stem cells
JOURNAL Patent: US 6576464-A 1 10-JUN-2003;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 397; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTGCTGGCTCCCTTGACCTTGGAGCGCGAGCGCGCGGGGAGCGCGC 60
Db 13148 CCCTGCTGGCTCCCTTGACCTTGGAGCGCGAGCGCGCGGGGAGCGCGC 13207
Qy 61 CCAGACCCCGGGTCCCGCGGAGAGCTGCGTGTGCGGGCGAGGCTCCAGTG 120
Db 13208 CCAGACCCCGGGTCCCGCGGAGAGCTGCGTGTGCGGGCGAGGCTCCAGTG 13267
Qy 121 GATTGCGGGGACAGAGCGCCAGAGCCCGCTTCCACAGTGGCGGAGGACTGGGGACCC 180
Db 13268 GATTGCGGGGACAGAGCGCCAGAGCCCGCTTCCACAGTGGCGGAGGACTGGGGACCC 13327
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Db 13328 GGGACACCGCTCTGCGCCCTTCACTTCCAGCTCCGCTCTCCGCGGAGACCCCGCCCG 13387
Qy 241 TCCGACCCCTTCCCGGGTCCCGGCGGCGAGCCCTTCCAGGCGCTTCCAGCCCTTCCCTT 300
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Qy 301 CTTTCCGGGCGCCCGCTCTCTCCGCGGCGAGTTTCAGGACGCGCTGCTGCT 360

Db 13448 CCTTTCGCGCGCCCGCTCTCTCCGCGCGGAGTTTCAGGACGCTGCTGCTGCT 13507
Qy 361 GCGCAGCTGGGAGCGCTTGGCCCGCGGCGACCCCGCG 397
Db 13508 GCGCAGCTGGGAGCGCTTGGCCCGCGGCGACCCCGCG 13544
RESULT 7
AR490112
LOCUS AR490112 15418 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 1 from patent US 6713055.
ACCESSION AR490112
VERSION AR490112.1 GI:47257268
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Schiff,J.M.
TITLE Glycosyltransferase vectors for treating cancer
JOURNAL Patent: US 6713055-A 1 30-MAR-2004;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 397; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 13268 GATTGCGGGGACAGAGCGCCAGAGCCCGCTTCCACAGTGGCGGAGGACTGGGGACCC 13327
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Db 13388 TCCGACCCCTTCCCGGGTCCCGGCGGCGAGCCCTTCCAGGCGCTTCCAGCCCTTCCCTT 13447
Qy 301 CTTTTCGCGCGCCCGCTCTCTCCGCGGCGAGTTTCAGGACGCGCTGCTGCT 360
Db 13448 CTTTTCGCGCGCCCGCTCTCTCCGCGGCGAGTTTCAGGACGCGCTGCTGCT 13507
Qy 361 GCGCAGCTGGGAGCGCTTGGCCCGCGGCGACCCCGCG 397
Db 13508 GCGCAGCTGGGAGCGCTTGGCCCGCGGCGACCCCGCG 13544

RESULT 8
AX453025
LOCUS AX453025 15418 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 1 from Patent WO0242445.
ACCESSION AX453025
VERSION AX453025.1 GI:21712594
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

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AUTHORS Gold,J.D. and Lebrowski,J.S.
TITLE Differentiated cells suitable for human therapy
JOURNAL Patent: WO 0242445-A 1 30-MAY-2002;
Geron Corporation (US)
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  Best Local Similarity 100.0%; Pred. No. 2.3e-49;
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  Db 13328 GGGCACCCCGTCCGCGCTTCCACCTTCCAGCTCCGCTCCCTCCGCGGAGCCCGCCCGCG 13387
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  LOCUS AX504952 15418 bp DNA linear PAT 27-SEP-2002
  DEFINITION Sequence 1 from Patent WO0242468.
  ACCESSION AX504952
  VERSION AX504952.1 GI:23386282
  KEYWORDS
  SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1
  AUTHORS Schiff,M.J.
  TITLE Glycosyltransferase vectors for treating cancer
  JOURNAL Patent: WO 0242468-A 1 30-MAY-2002;
  Geron Corporation (US)
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  DEFINITION Sequence 1 from Patent WO02053760.
  ACCESSION AX498409
  VERSION AX498409.1 GI:23343287
  KEYWORDS
  SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1
  AUTHORS Irving,J.M. and Lebrowski,J.S.
  TITLE Chimeric cytolytic viruses for cancer treatment
  JOURNAL Patent: WO 02053760-A 1 11-JUL-2002;
  Geron Corporation (US)
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VERSION .
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REFERENCE 1 (bases 1 to 92564)
Leem,S.H., Londono-Vallejo,J.A., Kim,J.H., Bui,H., Tubacher,B.,
Solomon,G., Park,J.E., Horikawa,I., Kouprina,N., Barrett,J.C. and
Larionov,V.
The human telomerase gene: complete genomic sequence and analysis
of tandem repeat polymorphisms in intronic regions
Oncogene 21 (5), 769-777 (2002)
JOURNAL
MEDLINE 21839826
PUBMED 11850805
REFERENCE 2 (bases 1 to 92564)
Londono-Vallejo,J.A.
Direct Submission
TITLE Submitted (06-SEP-2000) Centre d'Etudes du Polymorphisme Humain, 27
rue Juliette Dodu, Paris 75010, France
JOURNAL
REFERENCE 3 (bases 1 to 92564)
Londono-Vallejo,J.A.
Direct Submission
TITLE Submitted (10-OCT-2001) Centre d'Etudes du Polymorphisme Humain, 27
rue Juliette Dodu, Paris 75010, France
JOURNAL
REMARK Sequence update by submitter
COMMENT On Oct 10, 2001 this sequence version replaced gi:12642956.
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	DOE Joint Genome Institute.		
	Direct Submission		
	Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint		
	Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
	3 (bases 1 to 202305)		
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	Direct Submission		
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	Drive, Walnut Creek, CA 94598, USA		
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VERSION	AX003120.1	GI:9926982			
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AUTHORS	Wick, M. and Hagen, G.				
TITLE	Regulatory dna sequences of the human catalytic telomerase sub-unit gene, diagnostic and therapeutic use thereof				
JOURNAL	Patent: WO 9933998-A 1 08-JUL-1999;				
FEATURES	WICK MARESA (DE); BAYER AG (DE)				
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VERSION	AB016767.1	GI:4239869			
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ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 Takakura, M., Kyo, S., Kanaya, T., Hirano, H., Takeda, J., Yutsudo, M. and Inoue, M.				
TITLE	Cloning of human telomerase catalytic subunit (hTERT) gene promoter and identification of proximal core promoter sequences essential for transcriptional activation in immortalized and cancer cells				
JOURNAL	Cancer Res. 59 (3), 551-557(1999)				

MEDLINE	99137484	
PUBMED	9973199	
REFERENCE	2 (bases 1 to 5491)	
AUTHORS	Takakura,M., Kyo,S., Kanaya,T., Takeda,J. and Inoue,M.	
TITLE	Direct Submission	
JOURNAL	Submitted (04-AUG-1998) Mashiozo Takakura, Kanazawa University, School of Medicine, Department of Obstetrics and Gynecology; 13-1, Takaramachi, Kanazawa, Ishikawa 920-0934, Japan (E-mail:takakura@med.kanazawa-u.ac.jp, Tel:81-76-265-2425, Fax:81-76-264-4266)	
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 04:29:03 ; Search time 256.83 Seconds
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Title: US-10-081-969-94

Perfect score: 245

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	245	100.0	295	ABV75306	TERT mini
5	245	100.0	295	ABZ23897	TERT mini
6	245	100.0	455	ADI33422	Human tel
7	245	100.0	955	ABS98580	Ar17pAEzf
8	245	100.0	5126	AAH88272	Human cat
9	245	100.0	5928	ABK12707	Minimal t
10	245	100.0	51552	AAH96607	DNA encod
11	244	99.6	378	ACC47272	CEA gene
12	244	99.6	397	ABS98658	Human TER
13	244	99.6	408	ADR73423	Human tel
14	244	99.6	902	ADR73427	Human m-h
15	244	99.6	3962	AAH41091	Telomerases
16	244	99.6	15418	AAH63785	Nucleotid
17	244	99.6	15418	AAH63785	Human TER
18	244	99.6	15418	AAH38601	Human TER
19	244	99.6	15418	ABS54997	Lambda cl
20	244	99.6	15418	AAH38595	DNA of pl
	244	99.6	15418	ADC21253	Lambda cl

21	237.4	96.9	327	6	AAL55438	Specific
22	237.4	96.9	327	12	ADI80429	Anti-tumo
23	236	96.3	293	6	AAL55435	Specific
24	236	96.3	293	6	ABQ76069	Anticancer
25	229.8	93.8	314	3	AA94134	Telomerases
26	205	83.7	240	10	ABZ23898	Telomerases
27	205	83.7	454	11	ADN00285	Tumour-sp
28	201.2	82.1	35871	6	AAD27972	Recombina
29	201.2	82.1	35978	6	AAD27971	Recombina
30	200.8	82.0	403	6	ABS98583	Ar17pAEzf
31	199.8	81.6	4335	2	AAV16979	Human tel
32	198	80.8	1677	6	AAD27973	Human tel
33	183.2	74.8	4356	6	ABL92335	Chemical
34	158.6	64.7	1404	8	AAD22344	Chemical
35	144	58.8	144	8	ABZ79850	TERT mini
36	89	36.3	4356	6	ABL92334	Chemical
37	88	35.9	89	6	ABV73905	Telomerases
38	77	31.4	78	6	ABV74896	Minimal t
39	77	31.4	78	8	ABZ79851	Human slt
40	77	31.4	78	10	ABZ22591	Human TER
41	69.4	28.3	1404	6	AAD22343	Chemical
42	67	27.3	600	6	ABQ52497	Oligonucl
43	67	27.3	600	6	ABQ52496	Oligonucl
44	66.8	27.3	1416	8	ABZ20967	Animal te
45	66.6	27.2	28198	10	ADG37080	Mouse pla

ALIGNMENTS

RESULT 1

ABS98659

ID ABS98659 standard; DNA; 245 BP.

XX ABS98659;

AC ABS98659;

XX 17-DEC-2002 (first entry)

DT Human TERT promoter sequence #2.

DE Human TERT promoter sequence #2.

XX Virus; viral vector; adenoviral nucleic acid backbone; breast cancer;
inverted terminal repeat; ITR; termination signal sequence; lung cancer;
E2F responsive promoter; adenoviral packaging signal; prostate cancer;
neoplastic condition; colon cancer; cytostatic; immunostimulant;
gene therapy; human; TERT; promoter; ds.

OS Homo sapiens.

XX WO200267861-A2.

PN 06-SEP-2002.

PD 22-FEB-2002; 2002WO-US005300.

PF 23-FEB-2001; 2001US-0270922P.

XX 01-JUN-2001; 2001US-0295037P.

PR 14-JAN-2002; 2002US-0348670P.

XX (NOVS) NOVARTIS PHARMA AG.

PA Ennist DL, Forry-Schaudies S, Gorziglia M, Hallenbeck PL, Hay CM;

XX Jakubczak JL, Kaleko M, Ryan PC, Stewart DA, Xie Y, Connelly S;

PI Police SR, Clarke L, Phipps S, Cheng C;

XX WPI; 2002-705950/76.

DR Recombinant viral vector comprising an adenoviral nucleic acid backbone,

XX useful for treating neoplastic disorders such as lung, breast, prostate

PT or colon cancer.

XX Claim 11; Page 21; 226pp; English.

PS The present invention relates to a new recombinant viral vector

XX

CC

CC comprising an adenoviral nucleic acid backbone, where the backbone
CC comprises in sequential order, a left inverted terminal repeat (ITR), a
CC termination signal sequence, an E2F responsive promoter which is operably
CC linked to a gene essential for replication of the recombinant viral
CC vector, an adenoviral packaging signal and a right ITR. The methods and
CC compositions of the present invention are useful for treating a
CC neoplastic condition such as lung, breast, prostate or colon cancer. The
CC viral vectors are useful in studying methods of killing neoplastic cells
CC in vitro or in animal models. The present nucleic acid sequence
CC represents a human TERT promoter of the invention
XX
SQ Sequence 245 BP; 18 A; 127 C; 66 G; 34 T; 0 U; 0 Other;
Query Match 100.0%; Score 245; DB 6; Length 245;
Best Local Similarity 100.0%; Pred. No. 4.5e-34;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCACGTGGCGAGGAGCTGGGGACCCCGGGACCCCGTCTGCGCTTCACCTTCAGCT 60
Db 1 CCCACGTGGCGAGGAGCTGGGGACCCCGGGACCCCGTCTGCGCTTCACCTTCAGCT 60
QY 61 CGCGCTCTCCGCGGAGCCCGCCCGTCCCGACCCCTCCCGGTCGCCGCCAGCCC 120
Db 61 CGCGCTCTCCGCGGAGCCCGCCCGTCCCGACCCCTCCCGGTCGCCGCCAGCCC 120
QY 121 CCTCCGGGCTCCAGAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTCGCGGG 180
Db 121 CCTCCGGGCTCCAGAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTCGCGGG 180
QY 181 CGAGTTTCAGGACGCTGCTGCTGCGACAGTGGGAAGCCCTGGCGCCGACCC 240
Db 181 CGAGTTTCAGGACGCTGCTGCTGCGACAGTGGGAAGCCCTGGCGCCGACCC 240
QY 241 CC6CG 245
Db 241 CC6CG 245
RESULT 2
ID ABK12706 standard; DNA; 261 BP.
XX
AC ABK12706;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human telomerase reverse transcriptase (TERT) minimal promoter sequence.
XX
KW Human; telomerase reverse transcriptase; TERT; Site C; Progeria; burn;
KW repressor binding site; Hutchinson-Gilford syndrome; AIDS; cancer;
KW acquired immunodeficiency syndrome; cardiovascular disease; osteoporosis;
KW skin rejuvenation; immune senescence; bone marrow transplant; skin graft;
KW neoplastic disease; TERT minimal promoter; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 171..211
FT /tag= a
FT /label= Target site_C domain
FT /note= "Specifically claimed in claim 37"
FT 5'UTR 182..259
FT /tag= c
FT /note= "A portion of the 5' untranslated region"
FT misc_feature 182..209
FT /tag= b
FT /note= "Repressor site"
FT 190..210
FT /tag= e
FT /note= "Specifically claimed in claim 37"
FT misc_feature 190..202
FT /tag= d
FT /note= "Specifically claimed in claim 37"

FT misc_feature 191..201
FT /tag= f
FT /note= "E2F transcription factor binding site consensus
FT sequence, E2F-Q6"
FT misc_feature 192..201
FT /tag= g
FT /note= "Specifically claimed in claim 37"
XX
PN WO200216657-A1.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025861.
XX
PR 24-AUG-2000; 2000US-0227865P.
PR 01-SEP-2000; 2000US-0230174P.
PR 05-OCT-2000; 2000US-0238345P.
XX
XX (SIBR-) SIERRA SCI INC.
PI Andrews WH, Foster CA, Fraser S, Mohammadpour H;
XX WPI; 2002-280952/32.
DR
XX
PT Modulating expression of telomerase reverse transcriptase (TERT) in a
PT cell, for regulating proliferative capacity of a cell, involves
PT modulating TERT transcription repression by Site C repressor binding
PT site.
XX
PS Disclosure; Fig 1; 66pp; English.
XX
CC The present invention relates to a new method of modulating expression of
CC telomerase reverse transcriptase (TERT) from a TERT expression system
CC that includes a TERT promoter and a Site C repressor binding site. The
CC method of the invention involves modulating TERT transcription repression
CC by the Site C repressor binding site. The method of the invention is
CC useful for modulating expression of TERT for producing a mammalian
CC antibody. The method is also useful in a variety of different
CC applications, including immortalisation of cells, production of reagents
CC for use in life science research, therapeutic applications, and
CC therapeutic agent screening applications. Increasing TERT expression
CC delays natural telomeric shortening and/or increases telomeric length and
CC is useful for treating disease conditions such as Progeria or Hutchinson-
CC Gilford syndrome, acquired immunodeficiency syndrome (AIDS),
CC cardiovascular disease, osteoporosis, in skin rejuvenation and to inhibit
CC immune senescence. The method can be employed to lengthen telomeres of
CC osteoblast and osteoclast stem cells, encouraging bone replacement and
CC proper remodeling and reinforcement, and can thus be used in bone marrow
CC transplants for the treatment of cancer and skin grafts for burn victims
CC and as such the method improves the survival and effectiveness of bone
CC marrow and skin cell transplants. Decreasing TERT expression is useful
CC for treating cellular proliferative disease conditions, including
CC neoplastic disease conditions e.g. cancer. The present nucleic acid
CC sequence represents the human TERT minimal promoter sequence of the
CC invention
XX
SQ Sequence 261 BP; 21 A; 133 C; 71 G; 36 T; 0 U; 0 Other;
Query Match 100.0%; Score 245; DB 6; Length 261;
Best Local Similarity 100.0%; Pred. No. 4.4e-34;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCACGTGGCGAGGAGCTGGGGACCCCGGGACCCCGTCTGCGCTTCACCTTCAGCT 60
Db 14 CCCACGTGGCGAGGAGCTGGGGACCCCGGGACCCCGTCTGCGCTTCACCTTCAGCT 73
QY 61 CGCGCTCTCCGCGGAGCCCGCCCGTCCCGACCCCTCCCGGGTCGCCGCCAGCCC 120
Db 74 CGCGCTCTCCGCGGAGCCCGCCCGTCCCGACCCCTCCCGGGTCCCGGCCAGCCC 133
QY 121 CCTCCGGGCTCCAGAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTCGCGGG 180
Db 134 CCTCCGGGCTCCAGAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTCGCGGG 193

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Qy 181 CGAGTTTCAGGACGGCTGCGTCTGCTGCGACGTTGGGAAGCCCTGCGCCCGGCGCACCC 240
    |||||
Db 194 CGAGTTTCAGGACGGCTGCGTCTGCTGCGACGTTGGGAAGCCCTGCGCCCGGCGCACCC 253

Qy 241 CCGCG 245
    |||||
Db 254 CCGCG 258

RESULT 3
ABV75307
ID ABV75307 standard; DNA; 295 BP.
AC ABV75307;
XX
DT 07-MAR-2003 (first entry)
XX
DE Telomerase minimal promoter sequence.
XX
TERT; telomerase reverse transcriptase; TF-8; TF-13; telomerase;
KW cardiovascular; osteopathic; virucide; transcription; promoter; ds.
XX
OS Homo sapiens.
XX
PN WO200290570-A2.
XX
PD 14-NOV-2002.
XX
PF 07-MAY-2002; 2002WO-US014720.
XX
PR 08-MAY-2001; 2001US-0289717P.
XX
PA (SIER-) SIERRA SCI INC.
XX
PI Andrews WH;
XX
DR WPI; 2003-103520/09.
XX
PT New telomerase reverse transcriptase (TERT) TF-8 and/or TF-13 repressor
PT binding site, useful in regulating TERT expression and for screening
PT agents that modulate TERT transcription repressing activity of the TF-8
PT and TF-13 sites.
XX
PS Example; Page 31; 40pp; English.
XX
CC The invention relates to a new telomerase reverse transcriptase (TERT) TF
CC -8 and/or TF-13 repressor binding site. The nucleic acid comprising the
CC binding site sequence is useful in preparing constructs, such as vectors
CC and expression systems, and probes for the TERT TF-8 and/or TF-13
CC repressor binding site in non-human animals. Modulating the transcription
CC repressing activity of TERT TF-8 and/or TF-13 repressor factors to
CC regulate telomerase expression, can be used in immortalization of cells,
CC production of reagents useful in life science research, and therapeutic
CC research. Inhibitors of TERT transcription repression by a TF-8 and/or TF
CC -13 repressor may be used for increasing the proliferative capacity of a
CC cell, and for treating Progeria, Hutchinson-Gilford syndrome,
CC cardiovascular disease, osteoporosis, or AIDS. The present sequence
CC represents the telomerase minimal promoter
XX
SQ Sequence 295 BP; 26 A; 147 C; 81 G; 41 T; 0 U; 0 Other;

Query Match 100.0%; Score 245; DB 8; Length 295;
Best Local Similarity 100.0%; Pred. No. 4.3e-34;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCGCCCTTCCAGTTCACGCT 60
    |||||
Db 36 CCCACGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCGCCCTTCCAGTTCACGCT 95

Qy 61 CCGCTCTCTCCGCGGGACCCCGCGCTCCCGACCCCTCCCGGTTCCCGGCCCGAGCCC 120
    |||||
Db 96 CCGCTCTCTCCGCGGGACCCCGCGCTCCCGACCCCTCCCGGTTCCCGGCCCGAGCCC 155
```

```
Qy 121 CCTCCGGGCGCTCCACGCGCTCCCTTCTTTCGGGGCCCCCGCCCTCTCTCTCGCGCG 180
    |||||
Db 156 CCTCCGGGCGCTCCACGCGCTCCCTTCTTTCGGGGCCCCCGCCCTCTCTCTCGCGCG 215

Qy 181 CGAGTTTCAGGACGGCTGCGTCTGCTGCGACGTTGGGAAGCCCTGCGCCCGGCGCACCC 240
    |||||
Db 216 CGAGTTTCAGGACGGCTGCGTCTGCTGCGACGTTGGGAAGCCCTGCGCCCGGCGCACCC 275

Qy 241 CCGCG 245
    |||||
Db 276 CCGCG 280

RESULT 4
ABV75306
ID ABV75306 standard; DNA; 295 BP.
XX
AC ABV75306;
XX
DT 07-MAR-2003 (first entry)
XX
DE TERT minimal promoter sequence.
XX
TERT; telomerase reverse transcriptase; TF-8; TF-13; repressor;
KW cardiovascular; osteopathic; virucide; transcription; promoter; ds.
XX
OS Homo sapiens.
XX
PN WO200290570-A2.
XX
PD 14-NOV-2002.
XX
PF 07-MAY-2002; 2002WO-US014720.
XX
PR 08-MAY-2001; 2001US-0289717P.
XX
PA (SIER-) SIERRA SCI INC.
XX
PI Andrews WH;
XX
DR WPI; 2003-103520/09.
XX
PT New telomerase reverse transcriptase (TERT) TF-8 and/or TF-13 repressor
PT binding site, useful in regulating TERT expression and for screening
PT agents that modulate TERT transcription repressing activity of the TF-8
PT and TF-13 sites.
XX
PS Example; Page 28; 40pp; English.
XX
CC The invention relates to a new telomerase reverse transcriptase (TERT) TF
CC -8 and/or TF-13 repressor binding site. The nucleic acid comprising the
CC binding site sequence is useful in preparing constructs, such as vectors
CC and expression systems, and probes for the TERT TF-8 and/or TF-13
CC repressor binding site in non-human animals. Modulating the transcription
CC repressing activity of TERT TF-8 and/or TF-13 repressor factors to
CC regulate telomerase expression, can be used in immortalization of cells,
CC production of reagents useful in life science research, and therapeutic
CC research. Inhibitors of TERT transcription repression by a TF-8 and/or TF
CC -13 repressor may be used for increasing the proliferative capacity of a
CC cell, and for treating Progeria, Hutchinson-Gilford syndrome,
CC cardiovascular disease, osteoporosis, or AIDS. The present sequence
CC represents the TERT minimal promoter
XX
SQ Sequence 295 BP; 26 A; 147 C; 81 G; 41 T; 0 U; 0 Other;

Query Match 100.0%; Score 245; DB 8; Length 295;
Best Local Similarity 100.0%; Pred. No. 4.3e-34;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCGCCCTTCCAGTTCACGCT 60
    |||||
Db 36 CCCACGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCGCCCTTCCAGTTCACGCT 95
```


Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACAGTGGCGAGGAGTGGGGACCGGGACCCGTCCTGCCCCCTTACCTTCCAGCT 60
Db 211 CCCACAGTGGCGAGGAGTGGGGACCGGGACCCGTCCTGCCCCCTTACCTTCCAGCT 270

Qy 61 CCGCTCTCCGCGGAGCCCGCCCGTCCCGACCCCTCCGGGTCCCGGCCAGGCC 120
Db 271 CCGCTCTCCGCGGAGCCCGCCCGTCCCGACCCCTCCGGGTCCCGGCCAGGCC 330

Qy 121 CTTCCGGGCCCCCTCCAGCCCTTCCCTTCCGCGGCCCCCGCCCTCTCTCGCGCG 180
Db 331 CTTCCGGGCCCCCTCCAGCCCTTCCCTTCCGCGGCCCCCGCCCTCTCTCGCGCG 390

Qy 181 CGAGTTTCAGGAGCGCTGCGTCTGCTGCGCACTGGGAAGCCCTGCGGCCAGCC 240
Db 391 CGAGTTTCAGGAGCGCTGCGTCTGCTGCGCACTGGGAAGCCCTGCGGCCAGCC 450

Qy 241 CCGCG 245
Db 451 CCGCG 455

RESULT 7

ABS98580/c
ID ABS98580 standard; DNA; 955 BP.
XX
AC ABS98580;
XX
DT 29-AUG-2003 (revised)
DT 17-DEC-2002 (first entry)
XX

Arl7pAE2fTtrtex right end viral DNA sequence.

XX Virus: viral vector; adenoviral nucleic acid backbone; breast cancer;
KW inverted terminal repeat; ITR; termination signal sequence; lung cancer;
KW E2F responsive promoter; adenoviral packaging signal; prostate cancer;
KW neoplastic condition; colon cancer; cytostatic; immunostimulant;
KW gene therapy; ds.
XX
OS Viruses.
XX
PW WO200267861-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-US005300.
XX
PR 23-FEB-2001; 2001US-0270922P.
PR 01-JUN-2001; 2001US-0295037P.
PR 14-JAN-2002; 2002US-0348670P.
XX
PA (NOVS) NOVARTIS PHARMA AG.
XX
PI Ennist DL, Porry-Schaudies S, Gorziglia M, Hallenbeck PL, Hay CM;
PI Jakubczak JL, Kaleko M, Ryan PC, Stewart DA, Xie Y, Connelly S;
PI Police SR, Clarke L, Phipps S, Cheng C;
XX
DR WPI; 2002-706950/76.
XX

Recombinant viral vector comprising an adenoviral nucleic acid backbone,
useful for treating neoplastic disorders such as lung, breast, prostate
or colon cancer.
XX
XX Example 15; Fig 47; 226pp; English.

XX The present invention relates to a new recombinant viral vector
CC comprising an adenoviral nucleic acid backbone, where the backbone
CC comprises in sequential order, a left inverted terminal repeat (ITR), a
CC termination signal sequence, an E2F responsive promoter which is operably
CC linked to a gene essential for replication of the recombinant viral
CC vector, an adenoviral packaging signal and a right ITR. the methods and
CC compositions of the present invention are useful for treating a

CC neoplastic condition such as lung, breast, prostate or colon cancer. The
CC viral vectors are useful in studying methods of killing neoplastic cells
CC in vitro or in animal models. The present nucleic acid sequence
CC represents a viral DNA sequence that was used in the methods of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 955 BP; 266 A; 286 C; 236 G; 167 T; 0 U; 0 Other;

Query Match 100.0%; Score 245; DB 6; Length 955;
Best Local Similarity 100.0%; Pred. No. 3.6e-34;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACAGTGGCGAGGAGTGGGGACCGGGACCCGTCCTGCCCCCTTACCTTCCAGCT 60
Db 500 CCCACAGTGGCGAGGAGTGGGGACCGGGACCCGTCCTGCCCCCTTACCTTCCAGCT 441

Qy 61 CCGCTCTCCGCGGAGCCCGCCCGTCCCGACCCCTCCGGGTCCCGGCCAGGCC 120
Db 440 CCGCTCTCCGCGGAGCCCGCCCGTCCCGACCCCTCCGGGTCCCGGCCAGGCC 381

Qy 121 CTTCCGGGCCCCCTCCAGCCCTTCCCTTCCGCGGCCCCCGCCCTCTCTCGCGCG 180
Db 380 CTTCCGGGCCCCCTCCAGCCCTTCCCTTCCGCGGCCCCCGCCCTCTCTCGCGCG 321

Qy 181 CGAGTTTCAGGAGCGCTGCGTCTGCTGCGCACTGGGAAGCCCTGCGGCCAGCC 240
Db 320 CGAGTTTCAGGAGCGCTGCGTCTGCTGCGCACTGGGAAGCCCTGCGGCCAGCC 261

Qy 241 CCGCG 245
Db 260 CCGCG 256

RESULT 8

AAx88272
ID AAx88272 standard; DNA; 5126 BP.
XX
AC AAx88272;
XX
DT 22-SEP-1999 (first entry)
XX
DE Human catalytic telomerase subunit 5'-flanking regulatory DNA.
XX
KW Telomerase; subunit; human; regulatory; catalytic; anti-tumour; reporter;
KW modulator; telomerase regulatory region; cancer therapy; ss.
XX
OS Homo sapiens.
XX
PW DE19757984-A1.
XX
PD 01-JUL-1999.
XX
PF 24-DEC-1997; 97DE-01057984.
XX
PR 24-DEC-1997; 97DE-01057984.
XX
PA (FARB) BAYER AG.
XX
PI Hagen G, Wick M, Zubov D;
XX
DR WPI; 1999-372320/32.
XX
PT New 5' flanking regulatory sequence from the human catalytic telomerase
PT subunit gene useful for cancer therapy.
XX
PS Claim 1; Fig 4; 14pp; German.

XX This invention describes a novel 5' flanking regulatory sequence from the
CC human catalytic telomerase subunit gene. Recombinant constructs
CC containing the product of the invention can be linked with DNA encoding
CC an anti-tumour protein or reporter protein. The constructs are useful for
CC identifying candidate substances that modulate the activity of the
CC telomerase regulatory region. The constructs can be used in cancer

```
CC therapy
XX Sequence 5126 BP; 1009 A; 1532 C; 1404 G; 1180 T; 0 U; 1 Other;
SQ Query Match 100.0%; Score 245; DB 2; Length 5126;
Best Local Similarity 100.0%; Pred. No. 2.8e-34;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCAGTCGGCGAGGAGCTGGGGACCCCGGACCGTCTCCGCTTACCTTCCAGCT 60
DB 4879 CCCCAGTCGGCGAGGAGCTGGGGACCCCGGACCGTCTCCGCTTACCTTCCAGCT 4938

QY 61 CGGCTCTCTCCGCGGAGACCCCGCCCGGTCGCGAGACCCCTCCCGGGTCCCGGCCAGGCC 120
DB 4939 CGGCTCTCTCCGCGGAGACCCCGCCCGGTCGCGAGACCCCTCCCGGGTCCCGGCCAGGCC 4998

QY 121 CTTCCGGGCGCTTCCAGCCCTCCCTTCTTCTTCCGCGGCGCCGCTCTCTCCGGGG 180
DB 4999 CTTCCGGGCGCTTCCAGCCCTCCCTTCTTCTTCCGCGGCGCCGCTCTCTCCGGGG 5058

QY 181 CGAGTTTCAGGACGCTGGTCTCTGCGACGTTGGGAGCCCTGGCCCGGCCACCC 240
DB 5059 CGAGTTTCAGGACGCTGGTCTCTGCGACGTTGGGAGCCCTGGCCCGGCCACCC 5118

QY 241 CCGCG 245
DB 5119 CCGCG 5123

RESULT 9
ID ABK12707 standard; DNA; 5928 BP.
XX AC ABK12707;
XX 18-JUN-2002 (first entry)
XX Minimal telomerase promoter in plasmid designated pSSI20.
XX Human; telomerase reverse transcriptase; TERT; Site C; Progeria; burn;
KW repressor binding site; Hutchinson-Gilford syndrome; AIDS; cancer;
KW acquired immunodeficiency syndrome; cardiovascular disease; osteoporosis;
KW skin rejuvenation; immune senescence; bone marrow transplant; skin graft;
KW neoplastic disease; TERT minimal promoter; plasmid pSSI20; ss.
XX Homo sapiens.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
FH misc_feature 38..295
FT /tag= a
FT /note= "Telomerase minimal promoter"
FT misc_feature 295..310
FT /tag= b
FT /note= "Kozak fragment"
FT misc_feature 308..1864
FT /tag= c
FT /note= "Secreted Alkaline Phosphatase gene"
FT polyA_site 1860..2080
FT /tag= d
FT /standard_name= "PolyA addition site"
FT /note= "Late Poly-A addition site of SV40"
FT misc_feature 2394..2976
FT /tag= e
FT /note= "Bacterial origin of replication"
FT misc_feature 3170..4023
FT /tag= f
FT /note= "Ampicillin Resistance Gene, made sensitive by
mutagenesis"
FT misc_feature 4538..5196
FT /tag= g
FT /note= "Chloramphenicol Resistance Gene"
```

```
FT misc_feature 5217..5401
FT /tag= h
FT /note= "F1 Origin of Replication"
FT misc_feature 5768..5921
FT /tag= i
FT /note= "Transcription blocker"
XX WO200216657-A1.
XX 28-FEB-2002.
XX 17-AUG-2001; 2001WO-US025861.
XX 24-AUG-2000; 2000US-0227865P.
XX 01-SEP-2000; 2000US-0230174P.
XX 05-OCT-2000; 2000US-0238345P.
XX (STER-) SIERRA SCI INC.
XX Andrews WH, Foster CA, Fraser S, Mohammadpour H;
PI MPI; 2002-280952/32.
XX Modulating expression of telomerase reverse transcriptase (TERT) in a
cell, for regulating proliferative capacity of a cell, involves
modulating TERT transcription repression by Site C repressor binding
site.
XX Disclosure; Fig 2; 66pp; English.
XX The present invention relates to a new method of modulating expression of
telomerase reverse transcriptase (TERT) from a TERT expression system
that includes a TERT promoter and a Site C repressor binding site. The
method of the invention involves modulating TERT transcription repression
by the Site C repressor binding site. The method of the invention is
useful for modulating expression of TERT for producing a mammalian
antibody. The method is also useful in a variety of different
applications, including immortalisation of cells, production of reagents
for use in life science research, therapeutic applications, and
therapeutic agent screening applications. Increasing TERT expression
delays natural telomeric shortening and/or increases telomeric length and
is useful for treating disease conditions such as Progeria or Hutchinson-
Gilford syndrome, acquired immunodeficiency syndrome (AIDS),
cardiovascular disease, osteoporosis, in skin rejuvenation and to inhibit
immune senescence. The method can be employed to lengthen telomeres of
osteoblast and osteoclast stem cells, encouraging bone replacement and
proper remodeling and reinforcement, and can thus be used in bone marrow
transplants for the treatment of cancer and skin grafts for burn victims
and as such the method improves the survival and effectiveness of bone
marrow and skin cell transplants. Decreasing TERT expression is useful
for treating cellular proliferative disease conditions, including acid
neoplastic disease conditions e.g. cancer. The present nucleic acid
sequence represents plasmid SSI20 minimal telomerase promoter sequence.
This sequence contains part of the human TERT minimal promoter sequence
(ABK12706)
XX Sequence 5928 BP; 1445 A; 1607 C; 1541 G; 1335 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 245; DB 6; Length 5928;
Best Local Similarity 100.0%; Pred. No. 2.7e-34;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCAGTCGGCGAGGAGCTGGGGACCCCGGACCGTCTCCGCTTACCTTCCAGCT 60
DB 51 CCCCAGTCGGCGAGGAGCTGGGGACCCCGGACCGTCTCCGCTTACCTTCCAGCT 110

QY 61 CGGCTCTCTCCGCGGAGACCCCGCCCGGTCGCGAGACCCCTCCCGGGTCCCGGCCAGGCC 120
DB 111 CGGCTCTCTCCGCGGAGACCCCGCCCGGTCGCGAGACCCCTCCCGGGTCCCGGCCAGGCC 170

QY 121 CTTCCGGGCGCTTCCAGCCCTCCCTTCTTCTTCCGCGGCGCCGCTCTCTCCGGGG 180
DB 171 CTTCCGGGCGCTTCCAGCCCTCCCTTCTTCTTCCGCGGCGCCGCTCTCTCCGGGG 230
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Oy 181 CGAGTTTCAGCAGCGCTGCCTGCTGCTGCGCACGTGGGAAGCCCTGCCCGCCGCCACCC 240
    |||||
Db 231 CGAGTTTCAGCAGCGCTGCCTGCTGCTGCGCACGTGGGAAGCCCTGCCCGCCGCCACCC 290
    |||||
Oy 241 CCGCG 245
    |||||
Db 291 CCGCG 295
    |||||

RESULT 10
AAS96607
ID AAS96607 standard; DNA; 51552 BP.
XX AC
XX AC
XX DT
XX 09-APR-2002 (first entry)
XX DNA encoding human telomerase reverse transcriptase (TERT) #1.
XX Telomerase reverse transcriptase; TERT; cytotostatic; apoptosis;
KW cell growth inhibitor; antisense oligonucleotide; antisense technology;
KW ds.
XX Homo sapiens.
XX Key
FH Location/Qualifiers
FT 1..11492
FT exon /*tag= a
FT number= 1
FT 11274..47813
FT /*tag= b
FT /product= "TERT"
FT /note= "Telomerase reverse transcriptase"
FT 11493..11596
FT /*tag= c
FT number= 1
FT 11597..12950
FT /*tag= d
FT number= 2
FT 12951..21566
FT /*tag= e
FT number= 2
FT 21567..21762
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FT 24033..24719
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FT 24720..24899
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FT 24900..25393
FT /*tag= k
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FT 25394..25549
FT /*tag= l
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FT 25550..30195
FT /*tag= m
FT number= 6
FT 30196..30292
FT /*tag= n
FT number= 7
FT 30293..31272
FT /*tag= o
FT number= 7
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FT exon 31273..31358
    /*tag= p
    /number= 8
FT intron 31359..33843
    /*tag= q
    /number= 8
FT exon 33844..33957
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    /number= 9
FT intron 33958..35941
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    /*tag= t
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FT intron 36014..37884
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FT exon 37885..38073
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FT exon 41875..42001
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FT intron 42002..42881
    /*tag= y
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FT intron 46255..47035
    /*tag= ac
    /number= 14
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    /*tag= ae
    /number= 15
FT intron 47710..50544
    /*tag= af
    /number= 16
XX WO200188198-A1.
XX 22-NOV-2001.
XX 15-MAY-2001; 2001WO-US015774.
XX 16-MAY-2000; 2000US-00572423.
XX 07-DEC-2000; 2000US-00733294.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Gaarde WA, Freier SM, Wancewicz E;
XX WPI; 2002-075321/10.
XX P-PSDB; AAU72735.
XX New compound targeted to nucleic acid molecule encoding telomerase
    transcriptase (TERT), which specifically hybridizes with and inhibits
    expression of TERT, useful for modulating apoptosis and inhibiting cell
    growth.
XX
```

PS Example 19; Page 112-138; 154pp; English.

XX The invention describes a compound, 8-50 nucleobases in length targeted

CC to a nucleic acid molecule encoding human TERT (telomerase reverse

CC transcriptase), where the compound specifically hybridises with and

CC inhibits the expression of TERT. A series of oligonucleotides were

CC designed to target different regions of the human TERT RNA. These were 20

CC nucleotides in length and composed of a central gap region consisting of

CC ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by

CC five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-

CC MOE) nucleotides. The compounds were analysed for their effect on human

CC TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction

CC (PCR). The compound is useful for inhibiting the expression of TERT in

CC cells or tissues, for treating a human having disease or condition

CC associated with TERT, for modulating apoptosis, for inhibiting cell

CC growth (preferably, cancer cell growth), in antisense therapy and for

CC diagnostics and therapeutics. This sequence encodes human telomerase

CC reverse transcriptase (TERT) #1, and is used to create antisense

CC oligonucleotides which modify TERT expression, described in the method of

CC the invention

XX

SQ Sequence 51552 BP; 10709 A; 13313 C; 15370 G; 12158 T; 0 U; 2 Other;

Query Match 100.0%; Score 245; DB 6; Length 51552;

Best Local Similarity 100.0%; Pred. No. 1.9e-34;

Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCAGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCCCTTCCACCTTCCAGCT 60

Db 11029 CCCCAGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCCCTTCCACCTTCCAGCT 11088

QY 61 CCGCCTCTCTCCGGCGGAGACCCGCCGCCCTCCCGACCCCTCCGGGTCCCGGCCAGCCC 120

Db 11089 CCGCCTCTCTCCGGCGGAGACCCGCCGCCCTCCCGACCCCTCCGGGTCCCGGCCAGCCC 11148

QY 121 CTTCCGGGCGCTCCAGCCGCTCCCTTCTTCCGGGCGCCGCGCTCTCTCCGGGCG 180

Db 11149 CTTCCGGGCGCTCCAGCCGCTCCCTTCTTCCGGGCGCCGCGCTCTCTCCGGGCG 11208

QY 181 CGAGTTTCAGGACGCTGGTCTCTGTGGGACACGTGGGAGCCCTGGCCCGGCCACCC 240

Db 11209 CGAGTTTCAGGACGCTGGTCTCTGTGGGACACGTGGGAGCCCTGGCCCGGCCACCC 11268

QY 241 CCGCG 245

Db 11269 CCGCG 11273

RESULT 11

ACC47272

ID ACC47272 standard; DNA; 378 BP.

XX ACC47272;

XX

DT 11-AUG-2003 (first entry)

XX

DE CEA gene cis-acting sequence.

XX

XX Gene expression; promoter; cytostatic; gene therapy; antisense therapy;

XX cancer; cis-acting; CEA gene; ds.

XX

XX Unidentified.

OS

XX WO200313555-A1.

PN

XX 20-FEB-2003.

PD

XX 05-AUG-2002; 2002WO-US024741.

PF

XX 08-AUG-2001; 2001US-0310905P.

PR

XX (TEXA) UNIV TEXAS SYSTEM.

PA

XX

PI Fang B;

XX

DR WPI; 2003-256488/25.

XX

PT Expressing gene products in a cell type-preferential manner with a binary

PT or bicistronic expression system, useful for treating cancers of the

PT brain, head and neck, esophagus, thyroid, stomach, colon, liver,

PT prostate, skin and rectum.

XX

PS Disclosure; Page 139; 141pp; English.

XX

XX The invention relates to expressing gene product in a cell type-

CC preferential manner. The method involves providing a first expression

CC cassette having a cell type-preferential promoter, providing a second

CC expression cassette having an inducible promoter, and transferring the

CC first and second expression cassettes into a cell in which the cell type

CC -specific preferential promoter is active. The methods and compositions

CC of the present invention are useful for treating cancers of the brain,

CC head and neck, esophagus, thyroid, stomach, colon, liver, kidney,

CC prostate, breast, cervix, ovaries, testicles, rectum, skin and blood. The

CC present sequence represents a cis-acting sequence that confers expression

CC of the CEA gene

XX

SQ Sequence 378 BP; 35 A; 178 C; 121 G; 44 T; 0 U; 0 Other;

Query Match 99.6%; Score 244; DB 8; Length 378;

Best Local Similarity 100.0%; Pred. No. 6.2e-34;

Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCAGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCCCTTCCACCTTCCAGCT 60

Db 135 CCCCAGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCCCTTCCACCTTCCAGCT 194

QY 61 CCGCCTCTCTCCGGCGGAGACCCGCCGCCCTCCCGACCCCTCCGGGTCCCGGCCAGCCC 120

Db 195 CCGCCTCTCTCCGGCGGAGACCCGCCGCCCTCCCGACCCCTCCGGGTCCCGGCCAGCCC 254

QY 121 CTTCCGGGCGCTCCAGCCGCTCCCTTCTTCCGGGCGCCGCGCTCTCTCCGGGCG 180

Db 255 CTTCCGGGCGCTCCAGCCGCTCCCTTCTTCCGGGCGCCGCGCTCTCTCCGGGCG 314

QY 181 CGAGTTTCAGGACGCTGGTCTCTGTGGGACACGTGGGAGCCCTGGCCCGGCCACCC 240

Db 315 CGAGTTTCAGGACGCTGGTCTCTGTGGGACACGTGGGAGCCCTGGCCCGGCCACCC 374

QY 241 CCGC 244

Db 375 CCGC 378

RESULT 12

ABS98658

ID ABS98658 standard; DNA; 397 BP.

XX ABS98658;

XX

DT 17-DEC-2002 (first entry)

XX

DE Human TERT promoter sequence #1.

XX

XX Virus; viral vector; adenoviral nucleic acid backbone; breast cancer;

XX inverted terminal repeat; ITR; termination signal sequence; lung cancer;

XX E2F responsive promoter; adenoviral packaging signal; prostate cancer;

XX neoplastic condition; colon cancer; cytostatic; immunostimulant;

XX gene therapy; human; TERT; promoter; ds.

OS Homo sapiens.

XX

XX WO200267861-A2.

PN

XX 06-SEP-2002.

PD

XX 22-FEB-2002; 2002WO-US005300.

PF

```
XX 23-FEB-2001; 2001US-0270922P.
PR 01-JUN-2001; 2001US-0295037P.
PR 14-JAN-2002; 2002US-0348670P.
XX
PA (NOVS ) NOVARTIS PHARMA AG.
XX
PI Ennist DL, Forry-Schaudies S, Gorziglia M, Hallenbeck PL, Hay CM;
PI Jakubczak JL, Kaleko M, Ryan PC, Stewart DA, Xie Y, Connelly S;
PI Police SR, Clarke L, Phipps S, Cheng C;
XX
DR WPI; 2002-706950/76.
XX
PT Recombinant viral vector comprising an adenoviral nucleic acid backbone,
PT useful for treating neoplastic disorders such as lung, breast, prostate
PT or colon cancer.
XX
PS Claim 11; Page 21; 226pp; English.
XX
CC The present invention relates to a new recombinant viral vector
CC comprising an adenoviral nucleic acid backbone, where the backbone
CC comprises in sequential order, a left inverted terminal repeat (ITR), a
CC termination signal sequence, an E3F responsive promoter which is operably
CC linked to a gene essential for replication of the recombinant viral
CC vector, an adenoviral packaging signal and a right ITR. The methods and
CC compositions of the present invention are useful for treating a
CC neoplastic condition such as lung, breast, prostate or colon cancer. The
CC viral vectors are useful in studying methods of killing neoplastic cells
CC in vitro or in animal models. The present nucleic acid sequence
CC represents a human TERT promoter of the invention
XX
SQ Sequence 397 BP; 35 A; 186 C; 127 G; 49 T; 0 U; 0 Other;
Query Match 99.6%; Score 244; DB 6; Length 397;
Best Local Similarity 100.0%; Pred. No. 6.2e-34;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CCCACGTGGCGAGGACTGGGGACCCGGGACCCCGTCTGCCCCCTTACCTTCCAGTCTC 61
DB 154 CCCACGTGGCGAGGACTGGGGACCCGGGACCCCGTCTGCCCCCTTACCTTCCAGTCTC 213
QY 62 CGCTCTCTCCGGCGAGCCCGCCCGTCCCGACCCCTCCCGGTCCCGGCCAGCCCC 121
DB 214 CGCTCTCTCCGGCGAGCCCGCCCGTCCCGACCCCTCCCGGTCCCGGCCAGCCCC 273
QY 122 CTCGGGGCCCTCCAGCCCTCCCTCTCTTCCGCGCCCGCCCTCTCTCTCGGGCGGC 181
DB 274 CTCGGGGCCCTCCAGCCCTCCCTCTCTTCCGCGCCCGCCCTCTCTCTCGGGCGGC 333
QY 182 GAGTTTCAGGACGCTGCTCTGCTGCGCACGCTGGGAAGCCCTTGGCCCGGCCACCCC 241
DB 334 GAGTTTCAGGACGCTGCTCTGCTGCGCACGCTGGGAAGCCCTTGGCCCGGCCACCCC 393
QY 242 CGCG 245
DB 394 CGCG 397
RESULT 13
ADR73423
ID ADR73423 standard; DNA; 408 BP.
XX
AC ADR73423;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human telomerase reverse transcriptase (hTERT) gene promoter sequence.
XX
KW ds; cytosstatic; gene therapy; transcriptional regulatory sequence;
KW human telomere reverse transcriptase; hTERT; promoter;
KW c-Myc binding site; Sp1 binding site; cancer.
XX
OS Homo sapiens.
```

```
XX PN WO2004076668-A1.
XX
XX PD 10-SEP-2004.
XX
XX PF 27-FEB-2004; 2004WO-KR000427.
XX
XX PR 27-FEB-2003; 2003KR-00012364.
XX
XX PA (YUNC/) YUN C.
XX (KIMJ/) KIM J.
XX
XX PI Yun C, Kim J, Yang J;
XX
XX DR WPI; 2004-653423/63.
XX
XX PT New transcriptional regulatory sequence with a human telomere reverse
XX transcriptase promoter, useful for treating cancer, e.g. stomach, lung,
XX ovarian, liver, pancreatic, bladder, colon, cervical, breast, brain, or
XX head and neck cancer.
XX
XX PS Disclosure; SEQ ID NO 1; 130pp; English.
XX
XX CC The invention relates to a transcriptional regulatory sequence with a
XX human telomere reverse transcriptase (hTERT) promoter linked to a
XX nucleotide sequence comprising one or more c-Myc binding sites and/or one
XX or more Sp1 binding sites. The transcriptional regulatory sequence and
XX composition are useful for treating cancer, e.g. stomach, lung, ovarian,
XX liver, bronchogenic, nasopharyngeal, laryngeal, pancreatic, bladder,
XX colon, cervical, breast, brain, or head and neck cancer. This sequence
XX corresponds to the wild type human telomerase reverse transcriptase
XX (hTERT) promoter sequence used to generate the novel sequence of the
XX invention.
XX
XX SQ Sequence 408 BP; 35 A; 190 C; 132 G; 51 T; 0 U; 0 Other;
Query Match 99.6%; Score 244; DB 13; Length 408;
Best Local Similarity 100.0%; Pred. No. 6.2e-34;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CCCACGTGGCGAGGACTGGGGACCCGGGACCCCGTCTGCCCCCTTACCTTCCAGTCTC 61
DB 165 CCCACGTGGCGAGGACTGGGGACCCGGGACCCCGTCTGCCCCCTTACCTTCCAGTCTC 224
QY 62 CGCTCTCTCCCGCGGAGCCCGCCCGTCCCGACCCCTTCCCGGGTCCCGGCCAGCCCC 121
DB 225 CGCTCTCTCCCGCGGAGCCCGCCCGTCCCGACCCCTTCCCGGGTCCCGGCCAGCCCC 284
QY 122 CTCGGGGCCCTCCAGCCCTTCCCTTCTTCCGCGGCCCGCCCTCTCTCTCGGGGGGC 181
DB 285 CTCGGGGCCCTCCAGCCCTTCCCTTCTTCCGCGGCCCGCCCTCTCTCTCGGGGGGC 344
QY 182 GAGTTTCAGGACGCTGCTGCTGCGCACGCTGGGAAGCCCTTGGCCCGGCCACCCC 241
DB 345 GAGTTTCAGGACGCTGCTGCTGCGCACGCTGGGAAGCCCTTGGCCCGGCCACCCC 404
QY 242 CGCG 245
DB 405 CGCG 408
RESULT 14
ADR73427
ID ADR73427 standard; DNA; 902 BP.
XX
AC ADR73427;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human m-hTERT gene promoter sequence.
XX
KW ds; cytosstatic; gene therapy; transcriptional regulatory sequence;
KW human telomere reverse transcriptase; hTERT; promoter;
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c-Myc binding site; Sp1 binding site; cancer.
Homo sapiens.
Key
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/bound_moiety= "c-Myc protein"
228..236 /tag= b
/bound_moiety= "Sp1 transcription factor"
250..255 /tag= c
/bound_moiety= "Sp1 transcription factor"
282..290 /tag= d
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311..336 /tag= f
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381..386 /tag= g
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617..622 /tag= h
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672..680 /tag= i
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694..699 /tag= j
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775..780 /tag= m
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900 /tag= n
/note= "translation start site"

WO2004076668-A1.
10-SEP-2004.
27-FEB-2004; 2004WO-KR000427.
27-FEB-2003; 2003KR-00012364.
(YUNC/) YUN C.
(KIMJ/) KIM J.
Yun C, Kim J, Yang J;
WPI; 2004-653423/63.

New transcriptional regulatory sequence with a human telomere reverse transcriptase promoter, useful for treating cancer, e.g. stomach, lung, ovarian, liver, pancreatic, bladder, colon, cervical, breast, brain, or head and neck cancer.

Claim 6; SEQ ID NO 13; 130pp; English.

This invention relates to a transcriptional regulatory sequence with a human telomere reverse transcriptase (hTERT) promoter linked to a nucleotide sequence comprising one or more c-Myc binding sites and/or one

or more Sp1 binding sites. The transcriptional regulatory sequence and composition are useful for treating cancer, e.g. stomach, lung, ovarian, liver, bronchogenic, nasopharyngeal, laryngeal, pancreatic, bladder, colon, cervical, breast, brain, or head and neck cancer. This sequence corresponds to the modified human telomerase reverse transcriptase (hTERT) promoter sequence containing the extra c-Myc and Sp1 binding site sequences.

Sequence 902 BP; 103 A; 388 C; 282 G; 129 T; 0 U; 0 Other;
Query Match 99.6%; Score 244; DB 13; Length 902;
Best Local Similarity 100.0%; Pred. No. 5.4e-34;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CCCACGTGGCGAGGGAGTGGGGACCCGGGACCCGGTCTCTCCCTTCACTTCAGGTC 61
DB 171 CCCACGTGGCGAGGGAGTGGGGACCCGGGACCCGGTCTCTCCCTTCACTTCAGGTC 230
QY 62 GCCTCTCTCGGGGAGCCCGCCCGTCCGACCCCTCCGGGTCCCGGCCAGCCCC 121
DB 231 GCCTCTCTCGGGGAGCCCGCCCGTCCGACCCCTCCGGGTCCCGGCCAGCCCC 290
QY 122 CTCGGGCGCTCCCGACCCCTCCCTTCTTTCCGGGCGCCCGCCCTCTCTCTCGGGGCG 181
DB 291 CTCGGGCGCTCCCGACCCCTCCCTTCTTTCCGGGCGCCCGCCCTCTCTCTCGGGGCG 350
QY 182 GAGTTTCAGGAGCGCTCGTCTGCTGCGACAGTGGGAAGCCCTGGGCCCGGCCACCCC 241
DB 351 GAGTTTCAGGAGCGCTCGTCTGCTGCGACAGTGGGAAGCCCTGGGCCCGGCCACCCC 410
QY 242 CGCG 245
DB 411 CGCG 414

RESULT 15
AAH41091
ID AAH41091 standard; DNA; 3962 BP.
XX AC AAH41091;
XX 29-AUG-2001 (first entry)
XX Telomerase reverse transcriptase (TERT) DNA.
DE Phenotype switch molecule; phenotype-related gene battery;
KW gene localisation; telomere reverse transcriptase; TERT; ds.
XX Unidentified.
XX WO200138515-A1.
XX 31-MAY-2001.
XX 17-NOV-2000; 2000WO-CN000427.
XX 19-NOV-1999; 99CN-00121466.
XX (BIAN/) BIAN X.
XX BIAN X;
XX WPI; 2001-367684/38.

Isolating phenotype switch molecules and phenotype-related gene batteries from complex genomes of higher animals and plants, useful e.g. in gene localization and classification analysis.

Example 7; Page 27-29; 35pp; Chinese.

This invention relates to a method for isolating phenotype switch molecules and phenotype-related gene batteries from complex genomes of higher animals and plants. The method is useful in gene localisation and

CC classification analysis, studying gene development networks and function
CC networks, and designing drugs based on regulatory sequences of the
CC phenotypes for disease treatment. The present sequence represents DNA
CC encoding a telomere reverse transcriptase (TERT), which is used in an
CC example illustrating the use of the method of the invention
XX
SQ Sequence 3962 BP; 782 A; 1157 C; 1113 G; 910 T; 0 U; 0 Other;

Query Match		99.6%;	Score 244;	DB 4;	Length 3962;
Best Local Similarity		100.0%;	Pred. No. 4.3e-34;		
Matches 244;		Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	2	CCCACGTGCGGAGGACTGGGGACCGGGACCGGTCTGCCCCCTTACCTTCCAGCTC	61		
Db	3682	CCCCCGTGGCGAGGGACTGGGGACCGGGACCGGGACCGGTCTGCCCCCTTACCTTCCAGCTC	3741		
Qy	62	CGCCTCTCTCCGCGCGGACCGCCCGCTCCGACCCCTCCCGGGTCCCGGCCACAGCCCC	121		
Db	3742	CGCCTCTCTCCGCGCGGACCGCCCGCTCCGACCCCTCCCGGGTCCCGGCCACAGCCCC	3801		
Qy	122	CTCGGGGCGCTCCAGCCCGCTTCTTTTCGCGCCCGCCCTCTCTTCGCGGCGC	181		
Db	3802	CTCGGGGCGCTCCAGCCCGCTTCTTTTCGCGCCCGCCCTCTCTTCGCGGCGC	3861		
Qy	182	GAGTTTCAGGACGCGCTCGGTCTCTGCGACGCTGGGAAGCCCTGGGCCCGGCCACCCC	241		
Db	3862	GAGTTTCAGGACGCGCTCGGTCTCTGCGACGCTGGGAAGCCCTGGGCCCGGCCACCCC	3921		
Qy	242	CGCG	245		
Db	3922	CGCG	3925		

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SUMMARIES

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1	245	100.0	261	4 US-09-932-581-24	Sequence 24, Appl
2	245	100.0	5928	4 US-09-932-581-25	Sequence 25, Appl
3	245	100.0	44952	4 US-09-949-016-12197	Sequence 12197, A
4	245	100.0	44960	4 US-09-949-016-17583	Sequence 17583, A
5	245	100.0	51552	4 US-09-733-294A-30	Sequence 30, Appl
6	244	99.6	298	4 US-09-244-438-17	Sequence 17, Appl
7	244	99.6	4321	4 US-09-402-181B-6	Sequence 6, Appl
8	244	99.6	15418	4 US-09-783-203-1	Sequence 1, Appl
9	244	99.6	15418	4 US-09-994-427A-1	Sequence 1, Appl
10	244	99.6	15418	4 US-09-244-438-1	Sequence 1, Appl
11	229.8	93.8	314	4 US-09-916-510A-8	Sequence 8, Appl
12	204.4	83.4	4200	4 US-08-912-951-6	Sequence 6, Appl
13	201.2	82.1	35871	4 US-09-956-335-2	Sequence 2, Appl
14	201.2	82.1	35978	4 US-09-956-335-1	Sequence 1, Appl
15	199.8	81.6	4335	3 US-08-974-549A-6	Sequence 6, Appl
16	199.8	81.6	4335	4 US-09-721-456-6	Sequence 6, Appl
17	198	80.8	1677	4 US-09-956-335-3	Sequence 3, Appl
18	93.6	38.2	124	3 US-08-974-549A-726	Sequence 726, App
19	93.6	38.2	124	4 US-09-721-456-726	Sequence 726, App
20	77	31.4	78	4 US-09-932-581-7	Sequence 7, Appl
21	74	30.2	77	4 US-09-244-438-19	Sequence 19, Appl
22	74	30.2	89	4 US-09-244-438-20	Sequence 20, Appl
23	65.2	26.6	319	3 US-09-165-264-8	Sequence 8, Appl
24	64.6	26.4	320	3 US-09-165-264-7	Sequence 7, Appl
25	63.4	25.9	865	4 US-09-270-767-11042	Sequence 11042, A
26	62.8	25.6	320	3 US-09-165-264-14	Sequence 14, Appl
27	62.2	25.4	320	3 US-09-165-264-13	Sequence 13, Appl

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c	29	61.2	25.0	320	3	US-09-165-264-11	Sequence 11, Appl
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	32	57.2	23.3	12001	1	US-08-458-568A-11	Sequence 11, Appl
	33	57.2	23.3	152331	3	US-09-128-155-16	Sequence 16, Appl
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	35	55	22.4	3855	4	US-08-912-951-4	Sequence 4, Appl
	36	55	22.4	3855	4	US-09-402-181B-4	Sequence 4, Appl
	37	55	22.4	3855	4	US-09-721-456-4	Sequence 4, Appl
	38	55	22.4	4015	3	US-08-851-843A-224	Sequence 224, App
	39	55	22.4	4015	3	US-08-974-549A-1	Sequence 1, Appl
	40	55	22.4	4015	3	US-08-854-050-224	Sequence 224, App
	41	55	22.4	4015	3	US-09-430-323-224	Sequence 224, App
	42	55	22.4	4015	3	US-09-572-423B-3	Sequence 3, Appl
	43	55	22.4	4015	3	US-09-128-354-1	Sequence 1, Appl
	44	55	22.4	4015	3	US-09-675-321-1	Sequence 1, Appl
	45	55	22.4	4015	3	US-09-052-919-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-932-581-24
; Sequence 24, Application US/09932581
; Patent No. 6686159
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Foster, Christopher A.
; APPLICANT: Fraser, Stephanie
; APPLICANT: Mohammadpour, Hamid
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
; FILE REFERENCE: SIER-005
; CURRENT APPLICATION NUMBER: US/09/932.581
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/227,865
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/230,174
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/238,345
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 261
; TYPE: DNA
; ORGANISM: human
US-09-932-581-24

Query Match	100.0%	Score 245;	DB 4;	Length 261;
Best Local Similarity	100.0%;	Pred. No. 2.9e-41;		
Matches 245;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCCCACGTGCGGAGGAGTCTGGGACCCGGGACCCGCTCTGCTGCTTCCCTTCCAGCT	60	
Db	14	CCCCACGTGCGGAGGAGTCTGGGACCCGGGACCCGCTCTGCTGCTTCCCTTCCAGCT	73	
Qy	61	CGGCTCTCTCGCGGGGACCCGCGGCTCCGACCCCTCCGCGGCTCCCGGCCAGGCC	120	
Db	74	CGGCTCTCTCGCGGGGACCCGCGGCTCCGACCCCTCCGCGGCTCCCGGCCAGGCC	133	
Qy	121	CCTCGGGCCCTCCCGAGCCCTCCCTTCTTTCGCGGGCCCGCCCTCTCTCTCGGGCG	180	
Db	134	CCTCGGGCCCTCCCGAGCCCTCCCTTCTTTCGCGGGCCCGCCCTCTCTCTCGGGCG	193	
Qy	181	CGAGTTTCAGCAGCGTGTGCTGTGCTGCGACGTGGGAGCCCTGCGCCCGGCCACCC	240	
Db	194	CGAGTTTCAGCAGCGTGTGCTGTGCTGCGACGTGGGAGCCCTGCGCCCGGCCACCC	253	
Qy	241	CGCG 245		

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Db      254 CCGCG 258

RESULT 2
US-09-932-581-25
; Sequence 25, Application US/09932581
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6686159
; GENERAL INFORMATION:
; APPLICANT: Andrews, Christopher A.
; APPLICANT: Postler, Stephanie
; APPLICANT: Fraser, Stephanie
; APPLICANT: Mohammadpour, Hamid
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
; FILE REFERENCE: SIER-005
; CURRENT APPLICATION NUMBER: US/09/932,581
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/227,865
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/230,174
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/238,345
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic expression plasmid
US-09-932-581-25

Query Match      100.0%; Score 245; DB 4; Length 5928;
Best Local Similarity 100.0%; Pred. No. 2.8e-41;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCACGTGGCGAGGAGCTGGGGACCCGCGACCCGCTCTGCCCTTCCACCTTCCAGCT 60
Db      51 CCCACGTGGCGAGGAGCTGGGGACCCGCGACCCGCTCTGCCCTTCCACCTTCCAGCT 110

QY      61 CGCCTCTCCGCGCGGACCCGCGACCCGCTCTGCCCTTCCACCTTCCAGCT 120
Db      111 CGCCTCTCCGCGCGGAGCCGCGACCCGCTCTGCCCTTCCACCTTCCAGCT 170

QY      121 CTTCCGGGCCCCCAGCCGCTCTCTTCCGGGCCCCGCGCTCTCTCGGGCG 180
Db      171 CTTCCGGGCCCCCAGCCGCTCTCTTCCGGGCCCCGCGCTCTCTCGGGCG 230

QY      181 CGAGTTTCAGGACGCTGCTCTGCTGCGACGTTGGGAGCCCTTGGCCCGCCACCC 240
Db      231 CGAGTTTCAGGACGCTGCTGCTGCTGCGACGTTGGGAGCCCTTGGCCCGCCACCC 290

QY      241 CCGCG 245
Db      291 CCGCG 295

RESULT 3
US-09-949-016-12197
; Sequence 12197, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17583
; LENGTH: 44960
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(44960)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17583

Query Match      100.0%; Score 245; DB 4; Length 44960;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCACGTGGCGAGGAGCTGGGGACCCGCGGACCCGCTCTGCCCTTCCACCTTCCAGCT 60
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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12197
; LENGTH: 44952
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(44952)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12197

Query Match      100.0%; Score 245; DB 4; Length 44952;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCACGTGGCGAGGAGCTGGGGACCCGCGGACCCGCTCTGCCCTTCCACCTTCCAGCT 60
Db      1811 CCCACGTGGCGAGGAGCTGGGGACCCGCGGACCCGCTCTGCCCTTCCACCTTCCAGCT 1870

QY      61 CGCCTCTCTCCGCGCGGACCCGCGCTCCCGACCCCTCCCGGCTCCCGGCCACCCC 120
Db      1871 CGCCTCTCTCCGCGCGGACCCGCGCTCCCGACCCCTCCCGGCTCCCGGCCACCCC 1930

QY      121 CTTCCGGGCCCCCAGCCGCTCTCTTCCGGGCCCCGCGCTCTCTCGGGCG 180
Db      1931 CTTCCGGGCCCCCAGCCGCTCTCTTCCGGGCCCCGCGCTCTCTCGGGCG 1990

QY      181 CGAGTTTCAGGACGCTGCTGCTGCGACGTTGGGAGCCCTTGGCCCGCCACCC 240
Db      1991 CGAGTTTCAGGACGCTGCTGCTGCGACGTTGGGAGCCCTTGGCCCGCCACCC 2050

QY      241 CCGCG 245
Db      2051 CCGCG 2055

RESULT 4
US-09-949-016-17583
; Sequence 17583, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17583
; LENGTH: 44960
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(44960)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17583

Query Match      100.0%; Score 245; DB 4; Length 44960;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCACGTGGCGAGGAGCTGGGGACCCGCGGACCCGCTCTGCCCTTCCACCTTCCAGCT 60
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Db 1811 CCCACGTGGCGAGGAGTGGGACCCGGGACCCGGCTCTGCCCCCTTACCTTCCAGCT 1870
Qy 61 CCGCTCTCTCCGCGGAGACCCCGCCGCTCCCGACCCCTCCCGGGTCCCGGGCCAGGCC 120
Db 1871 CCGCTCTCTCCGCGGAGACCCCGCCGCTCCCGACCCCTCCCGGGTCCCGGGCCAGGCC 1930
Qy 121 CCTCGGGCCCTCCAGACCCCTCCCTTCTCTTTCGGGGCCCGCCCTCTCTCTCGGGCG 180
Db 1931 CCTCGGGCCCTCCAGACCCCTCCCTTCTCTTTCGGGGCCCGCCCTCTCTCTCGGGCG 1990
Qy 181 CGAGTTTCAGGACGCTGCTCTCTGCGCAGCTGGGAGCCCTGGCCCGGCCACCC 240
Db 1991 CGAGTTTCAGGACGCTGCTCTCTGCGCAGCTGGGAGCCCTGGCCCGGCCACCC 2050
Qy 241 CCGCG 245
Db 2051 CCGCG 2055

RESULT 5
US-09-733-294A-30
; Sequence 30, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Preler
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733.294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572.423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 30
; LENGTH: 51552
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)...(11492)
; OTHER INFORMATION: exon 1
; NAME/KEY: intron
; LOCATION: (11493)...(11596)
; OTHER INFORMATION: intron 1
; NAME/KEY: exon
; LOCATION: (11597)...(12950)
; OTHER INFORMATION: exon 2
; NAME/KEY: intron
; LOCATION: (12951)...(21566)
; OTHER INFORMATION: intron 2
; NAME/KEY: exon
; LOCATION: (21567)...(21762)
; OTHER INFORMATION: exon 3
; NAME/KEY: intron
; LOCATION: (21763)...(23851)
; OTHER INFORMATION: intron 3
; NAME/KEY: exon
; LOCATION: (23852)...(24032)
; OTHER INFORMATION: exon 4
; NAME/KEY: intron
; LOCATION: (24033)...(24719)
; OTHER INFORMATION: intron 4
; NAME/KEY: exon
; LOCATION: (24720)...(24899)
; OTHER INFORMATION: exon 5
; NAME/KEY: intron
; LOCATION: (24900)...(25393)
; OTHER INFORMATION: intron 5
; NAME/KEY: exon
; LOCATION: (25394)...(25549)

; OTHER INFORMATION: exon 6
; NAME/KEY: intron
; LOCATION: (25550)...(30196)
; OTHER INFORMATION: intron 6
; NAME/KEY: exon
; LOCATION: (30195)...(30292)
; OTHER INFORMATION: exon 7
; NAME/KEY: intron
; LOCATION: (30293)...(31272)
; OTHER INFORMATION: intron 7
; NAME/KEY: exon
; LOCATION: (31273)...(31358)
; OTHER INFORMATION: exon 8
; NAME/KEY: intron
; LOCATION: (31359)...(33843)
; OTHER INFORMATION: intron 8
; NAME/KEY: unsure
; LOCATION: 31450
; OTHER INFORMATION: unknown
; NAME/KEY: exon
; LOCATION: (33844)...(33957)
; OTHER INFORMATION: exon 9
; NAME/KEY: intron
; LOCATION: (33958)...(35941)
; OTHER INFORMATION: intron 9
; NAME/KEY: exon
; LOCATION: (35942)...(36013)
; OTHER INFORMATION: exon 10
; NAME/KEY: intron
; LOCATION: (36014)...(37884)
; OTHER INFORMATION: intron 10
; NAME/KEY: exon
; LOCATION: (37885)...(38073)
; OTHER INFORMATION: exon 11
; NAME/KEY: intron
; LOCATION: (38074)...(41874)
; OTHER INFORMATION: intron 11
; NAME/KEY: exon
; LOCATION: (41875)...(42001)
; OTHER INFORMATION: exon 12
; NAME/KEY: intron
; LOCATION: (42002)...(42881)
; OTHER INFORMATION: intron 12
; NAME/KEY: exon
; LOCATION: (42882)...(42943)
; OTHER INFORMATION: exon 13
; NAME/KEY: intron
; LOCATION: (42944)...(46129)
; OTHER INFORMATION: intron 13
; NAME/KEY: exon
; LOCATION: (46130)...(46254)
; OTHER INFORMATION: exon 14
; NAME/KEY: intron
; LOCATION: (46255)...(47035)
; OTHER INFORMATION: intron 14
; NAME/KEY: exon
; LOCATION: (47036)...(47173)
; OTHER INFORMATION: exon 15
; NAME/KEY: intron
; LOCATION: (47174)...(47709)
; OTHER INFORMATION: intron 15
; NAME/KEY: exon
; LOCATION: (47710)...(50544)
; OTHER INFORMATION: exon 16
; US-09-733-294A-30

Query Match 100.0%; Score 245; DB 4; Length 51552;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACGTGGCGGAGGAGTGGGACCCGGGACCCGGCTCTGCCCCCTTACCTTCCAGCT 60
Db 11029 CCCACGTGGCGGAGGAGTGGGACCCGGGACCCGGCTCTGCCCCCTTACCTTCCAGCT 11088


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Query Match          99.6%; Score 244; DB 4; Length 4321;
Best Local Similarity 100.0%; Pred. No. 4.4e-41;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCAGTGGCGGAGGAGTGGGGACCCGGGACCCGGGACCCGGTCTGCGCCCTTACACCTTCCAGGTC 61
Db 2239 CCCAGTGGCGGAGGAGTGGGGACCCGGGACCCGGGACCCGGTCTGCGCCCTTACACCTTCCAGGTC 2298

QY 62 CGCTCTCTCCGGCGGAGACCCCGCCCGTCCCGACCCCTTCCGGGTCCCGGGCCAGCCCC 121
Db 2299 CGCTCTCTCCGGCGGAGACCCCGCCCGTCCCGACCCCTTCCGGGTCCCGGGCCAGCCCC 2358

QY 122 CTCGGGGCCCTCCAGCCCTCCCTTCTTTCCGGGGCCCGCCCTCTCTCGGGGGC 181
Db 2359 CTCGGGGCCCTCCAGCCCTCCCTTCTTTCCGGGGCCCGCCCTCTCTCGGGGGC 2418

QY 182 GAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGCCCTGGCCCGGCCACCCC 241
Db 2419 GAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGCCCTGGCCCGGCCACCCC 2478

QY 242 CGCG 245
Db 2479 CGCG 2482

RESULT 8
US-09-783-203-1
; Sequence 1, Application US/09783203
; Patent No. 6576464
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tpacked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/09/783,203
; CURRENT FILING DATE: 2001-02-13
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-783-203-1
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Query Match          99.6%; Score 244; DB 4; Length 15418;
Best Local Similarity 100.0%; Pred. No. 4.4e-41;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCAGTGGCGGAGGAGTGGGGACCCGGGACCCGGGACCCGGTCTGCGCCCTTACACCTTCCAGGTC 61
Db 13301 CCCAGTGGCGGAGGAGTGGGGACCCGGGACCCGGGACCCGGTCTGCGCCCTTACACCTTCCAGGTC 13360

QY 62 CGCTCTCTCCGGCGGAGACCCCGCCCGTCCCGACCCCTTCCGGGTCCCGGGCCAGCCCC 121
Db 13361 CGCTCTCTCCGGCGGAGACCCCGCCCGTCCCGACCCCTTCCGGGTCCCGGGCCAGCCCC 13420

QY 122 CTCGGGGCCCTCCAGCCCTCCCTTCTTTCCGGGGCCCGCCCTCTCTCGGGGGC 181
Db 13421 CTCGGGGCCCTCCAGCCCTCCCTTCTTTCCGGGGCCCGCCCTCTCTCGGGGGC 13480

QY 182 GAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGCCCTGGCCCGGCCACCCC 241
Db 13481 GAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGCCCTGGCCCGGCCACCCC 13540

QY 242 CGCG 245
Db 13541 CGCG 13544
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RESULT 9
US-09-994-427A-1
; Sequence 1, Application US/09994427A
; Patent No. 6713055
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
; FILE REFERENCE: 083,002
; CURRENT APPLICATION NUMBER: US/09/994,427A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/253,395
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-994-427A-1
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Query Match          99.6%; Score 244; DB 4; Length 15418;
Best Local Similarity 100.0%; Pred. No. 4.4e-41;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCAGTGGCGGAGGAGTGGGGACCCGGGACCCGGGACCCGGTCTGCGCCCTTACACCTTCCAGGTC 61
Db 13301 CCCAGTGGCGGAGGAGTGGGGACCCGGGACCCGGGACCCGGTCTGCGCCCTTACACCTTCCAGGTC 13360

QY 62 CGCTCTCTCCGGCGGAGACCCCGCCCGTCCCGACCCCTTCCGGGTCCCGGGCCAGCCCC 121
Db 13361 CGCTCTCTCCGGCGGAGACCCCGCCCGTCCCGACCCCTTCCGGGTCCCGGGCCAGCCCC 13420

QY 122 CTCGGGGCCCTCCAGCCCTCCCTTCTTTCCGGGGCCCGCCCTCTCTCGGGGGC 181
Db 13421 CTCGGGGCCCTCCAGCCCTCCCTTCTTTCCGGGGCCCGCCCTCTCTCGGGGGC 13480

QY 182 GAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGCCCTGGCCCGGCCACCCC 241
Db 13481 GAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGCCCTGGCCCGGCCACCCC 13540

QY 242 CGCG 245
Db 13541 CGCG 13544
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RESULT 10
US-09-244-438-1
; Sequence 1, Application US/09244438
; Patent No. 6777203
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; TITLE OF INVENTION: Regulatory Sequences and Methods of Using
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/09/244,438
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-09-244-438-1
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Query Match          99.6%; Score 244; DB 4; Length 15418;
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Best Local Similarity 100.0%; Pred. No. 4.4e-41;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCAGTGGCGAGGAGCTGGGGACCCGGGACCGCTCTGCGCCCTTACCTTCCAGCTC 61
Db 13301 CCCAGTGGCGAGGAGCTGGGGACCCGGGACCGCTCTGCGCCCTTACCTTCCAGCTC 13360

QY 62 CGCTCTCTCCGGCGGAGACCCCGCGCTGCTGCGACCCCTCCCGGGTCCCGGGCCAGCCCC 121
Db 13361 CGCTCTCTCCGGCGGAGACCCCGCGCTGCTGCGACCCCTCCCGGGTCCCGGGCCAGCCCC 13420

QY 122 CTCGGGCGCTCCAGCCCTCCCTTCTTCCGGGGCCCGCGCTCTCTCTCGGGGCGC 181
Db 13421 CTCGGGCGCTCCAGCCCTCCCTTCTTCCGGGGCCCGCGCTCTCTCTCGGGGCGC 13480

QY 182 GAGTTTCAGGACGCTGCGTCTGTCGACGCTGGGAAGCCCTGGCCCCCGCCACCCC 241
Db 13481 GAGTTTCAGGACGCTGCGTCTGTCGACGCTGGGAAGCCCTGGCCCCCGCCACCCC 13540

QY 242 CGCG 245
Db 13541 CGCG 13544

RESULT 11
US-09-916-510A-8
; Sequence 8, Application US/09916510A
; Patent No. 6544507
; GENERAL INFORMATION:
; APPLICANT: IGO, RICHARD D.
; APPLICANT: BRUNORI, MICHELE A.
; TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
; FILE REFERENCE: 604-596
; CURRENT APPLICATION NUMBER: US/09/916,510A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: GB 9906815.7
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-916-510A-8

Query Match 93.8%; Score 229.8; DB 4; Length 314;
Best Local Similarity 98.8%; Pred. No. 3.4e-38;
Matches 242; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 CCCACGTGGCGAGGAGCTGGGGACCCGGGACCCCGTCTGCGCCCTTACCTTCCAGCT 60
Db 71 CCCACGTGGCGAGGAGCTGGGGACCCGGGACCCCGTCTGCGCCCTTACCTTCCAGCT 130

QY 61 CGCTCTCTCCGGCGGAGCCCGCCCGCTCCGACCCCTCCGGGTCCCGGCCAGGCC 120
Db 131 CGCTCTCTCCGGCGGAGCCCGCCCGCTCCGACCCCTCCGGGTCCCGGCCAGGCC 190

QY 121 CTCTCGGGGCTCCAGCCCTCCCTCTCTTTCGGGGCCCGCGCTCTCTCTCGGGCG 180
Db 191 CTCTCGGG-CTTCCAGCCCGCCCTTCTTTCGGGGCCCGCGCTCTCTCTCGGGCG 249

QY 181 CGAGTTTCAGGACGCTGCTGCTGCGACAGTGGGAAGCCCTGGCCCCCGGCCACCC 240
Db 250 CGAGTTTCAGGACGCTGCTGCTGCGACAGTGGGAAGCCCTGGCCCCCGGCCACCC 309

QY 241 CGCG 245
Db 310 CGCG 314

RESULT 12
US-08-912-951-6
; Sequence 6, Application US/08912951

; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-912-951-6

Query Match 83.4%; Score 204.4; DB 4; Length 4200;
Best Local Similarity 94.7%; Pred. No. 4.5e-33;
Matches 233; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 2 CCCACGTGGCGAGGAGCTGGGGACCCGGGACCCCGTCTGCGCCCTTACCTTCCAGCTC 61
Db 2067 CCCACGTGGCGAAGAGCTGGGGACCCCGGACCCCGTCTGCGCCCTTACCTTCCAGCTC 2126

QY 62 CGCTCTCTCCGGCGGAGACCCCGCGCTGCTCCGACCCCTCCCGGGTCCCGGCCAGCCCC 121
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Db	2127	CGCTTTCCGCGCGGACCGCGCGCTCCGAAACCTTCCAGGTTCCGCGCCAGCGCC	2186
Qy	122	CTCCGGGCGCTCCAGCCCTCCCTTTCC- TTTTCGCGCGCCCGCGCTCTCC-TCGCGGC	179
Db	2187	TTCCGGGCGCTCCAGCCCTCCCTTTCCCTTTTCGCGCGCCCGCGCTCTCTCTTCGCGC	2246
Qy	180	GCAGTTTTCAGGCGCGCTGCGTCTGCTGCGCACGTGGGAAAGCCCTGGCCCCCGGCACC	239
Db	2247	GCGAGTTTTCAGGCGCGCTGCGTCTGCTGCGCACGTGGGAAAGCCCTGGCCCCCGGCACC	2306
Qy	240	CCCGCG 245	
Db	2307	CCCGCG 2312	

RESULT 13

US-09-956-335-2/c

; Sequence 2, Application US/09956335

; Patent No. 6627190

; GENERAL INFORMATION:

; APPLICANT: WOLD, William

; APPLICANT: TOY, Karoly

; APPLICANT: KUPPASWAMI, Mohan

; APPLICANT: DORONIN, Konsantin

; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE

; FILE REFERENCE: 16153-8394

; CURRENT APPLICATION NUMBER: US/09/956,335

; CURRENT FILING DATE: 2001-09-19

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 35871

; TYPE: DNA

; ORGANISM: Adenovirus

US-09-956-335-2

Query Match 82.1%; Score 201.2; DB 4; Length 35871;

Best Local Similarity 98.5%; Pred. No. 2e-32;

Matches 203; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	2	CCACGTTGCGGAGGACTGGGACCCGGGACCCGTCCTGTCGCGCTTACCTTCCAGTTC	61
Db <td>34232</td> <td>CCACGTTGCGGAGGACTGGGACCCGGGACCCGTCCTGTCGCGCTTACCTTCCAGTTC</td> <td>34173</td>	34232	CCACGTTGCGGAGGACTGGGACCCGGGACCCGTCCTGTCGCGCTTACCTTCCAGTTC	34173
Qy <td>62</td> <td>CGCTCTCTCGCGCGGACCCCGCGCTCCGACCCCTCCCGGTCCTCCGCGCCAGCGCC</td> <td>121</td>	62	CGCTCTCTCGCGCGGACCCCGCGCTCCGACCCCTCCCGGTCCTCCGCGCCAGCGCC	121
Db <td>34172</td> <td>CGCTCTCTCGCGCGGACCCCGCGCTCCGACCCCTCCCGGTCCTCCGCGCCAGCGCC</td> <td>34113</td>	34172	CGCTCTCTCGCGCGGACCCCGCGCTCCGACCCCTCCCGGTCCTCCGCGCCAGCGCC	34113
Qy <td>122</td> <td>CTCGGGGCTCCCGAGCCCTCCCTTCTCTTTTCGCGGGCCCGCGCTCTCTCTCGCGGGC</td> <td>181</td>	122	CTCGGGGCTCCCGAGCCCTCCCTTCTCTTTTCGCGGGCCCGCGCTCTCTCTCGCGGGC	181
Db <td>34112</td> <td>CTCGGGGCTCCCGAGCCCTCCCTTCTCTTTTCGCGGGCCCGCGCTCTCTCTCGCGGGC</td> <td>34053</td>	34112	CTCGGGGCTCCCGAGCCCTCCCTTCTCTTTTCGCGGGCCCGCGCTCTCTCTCGCGGGC	34053
Qy <td>182</td> <td>GAGTTTTCAGGCGCGTGGCTCTGTC 207</td> <td></td>	182	GAGTTTTCAGGCGCGTGGCTCTGTC 207	
Db <td>34052</td> <td>GAGTTTTCAGGCGCGTGGCTCTGTC 34027</td> <td></td>	34052	GAGTTTTCAGGCGCGTGGCTCTGTC 34027	

RESULT 14

US-09-956-335-1/c

; Sequence 1, Application US/09956335

; Patent No. 6627190

; GENERAL INFORMATION:

; APPLICANT: WOLD, William

; APPLICANT: TOY, Karoly

; APPLICANT: KUPPASWAMI, Mohan

; APPLICANT: DORONIN, Konsantin

; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE

; FILE REFERENCE: 16153-8394

; CURRENT APPLICATION NUMBER: US/09/956,335

; CURRENT FILING DATE: 2001-09-19

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/ FILING DATE: 09-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/17618
/ FILING DATE: 01-OCT-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph Ted
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4335 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: -
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/ OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
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Query Match      81.6%; Score 199.8; DB 3; Length 4335;
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Matches 237; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

QY      2  CCCACGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCCCCCTTCACCTTCAGCTC 61
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QY      62  CGCCTCTCCGCGCGG-ACCCGCGCCGCTCCCG-ACCCCTCCCGGTCCCGGCCAGCC 119
Db      2309  CGCCTCTCCGCGCGGAAACCCGCGCCGCTCCCGAACCTTCCTCGGTCCCGGCCAGCC 2368

QY      120  CCCTCCGGGCGCTCCAGCCCTTCCCTTCC-TTTCGGGCGCCCGCCCTCTCTCGCGG 178
Db      2369  CCTTCGGGGCCATCCAGCCGCTCCCGTTCTTTTCGGGCGCCCGCCCTCTCTCGCGG 2428

QY      179  CGCGAGTTTCAGGACGCTGCGTCTGTGTCGACGTGGGAAGCCCTGGCCCCCGGCCAC 238
Db      2429  CGCGAGTTTCAGGACGCTGCGTCTGTGTCGACGTGGGAAGCCCTGGCCCCCGGCCAC 2488

QY      239  CCCCCG 245
Db      2489  CCCCCG 2495
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Job time : 78.8505 secs

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 05:34:49 ; Search time 1229.58 Seconds
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Title: US-10-081-969-94
Perfect score: 245
Sequence: 1 cccacgtggcggaggact.....tggcccgccacccccgcg 245

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
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Listing first 45 summaries

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5: gb_ov.*
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7: gb_ph.*
8: gb_pl.*
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10: gb_to.*
11: gb_str.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245	100.0	245	6	AX817858 Sequence
2	245	100.0	261	6	AR455896 Sequence
3	245	100.0	955	6	AX817781 Sequence
4	245	100.0	5126	6	AX003120 Sequence
5	245	100.0	5491	9	AB016767 Sequence
6	245	100.0	5928	6	AR455897 Sequence
7	245	100.0	11276	6	AX003122 Sequence
8	245	100.0	26414	9	HS1871 Sequence
9	245	100.0	51552	6	AR266023 Sequence
10	244	99.6	397	6	AX817857 Sequence
11	244	99.6	2043	9	AF098956 Sequence
12	244	99.6	4321	6	AR390473 Sequence
13	244	99.6	4356	9	AF097365 Sequence
14	244	99.6	15332	9	AF121948 Homo sapi
15	244	99.6	15418	6	AR342806 Sequence
16	244	99.6	15418	6	AR490112 Sequence
17	244	99.6	15418	6	AX453025 Sequence
18	244	99.6	15418	6	AX498409 Sequence
19	244	99.6	15418	6	AX504952 Sequence

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c 23	233	95.1	170646	2	AC123545 Pan trogl
24	229.8	93.8	314	6	BD262062 Antineopl
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27	229.8	93.8	12213	9	AF114847 Homo sapi
28	229	93.5	2132	9	AF325900 Homo sapi
29	205	83.7	1404	9	AB018788 Homo sapi
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c 31	201.2	82.1	35871	6	AR403724 Sequence
c 32	201.2	82.1	35978	6	AR403723 Sequence
c 33	200.8	82.0	403	6	AX817785 Sequence
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35	199.8	81.6	4335	6	AR393087 Sequence
36	199.8	81.6	4335	6	AX810041 Sequence
37	199.8	81.6	4335	6	BD011047 Human tel
c 38	198	80.8	1677	6	AR403725 Sequence
c 39	186	75.9	170946	2	AC117933 Papio anu
c 40	186	75.9	183506	2	AC122155 Papio anu
c 41	183.2	74.8	4356	6	AX356510 Sequence
c 42	158.6	64.7	1404	6	AX280012 Sequence
43	93.6	38.2	124	6	AR393446 Sequence
44	89	36.3	4356	6	AX356509 Sequence
45	77	31.4	78	6	AR455879 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AX817858 245 bp DNA linear PAT 10-DEC-2003
DEFINITION Sequence 94 from Patent WO02067861.
ACCESSION AX817858
VERSION AX817858.1 GI:39723053
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Oncolytic adenoviral vectors
TITLE Patent: WO 02067861-A 94 06-SBP-2002;
JOURNAL Location/Qualifiers
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1..245
/organism="Homo sapiens"
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1..245
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	Best Local Similarity	100.0%;	Pred. No. 4.8e-29;						
	Matches 245;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	CCCCACGTGGCGAGGACTGGGGACCCGGGACCCGTCCTGCCCCCTTCACCTTCAGCT	60						
Db	1	CCCCACGTGGCGAGGACTGGGGACCCGGGACCCGTCCTGCCCCCTTCACCTTCAGCT	60						
QY	61	CGGCTCTCTCCGGCGGACCCCGCCCCGTCGCGACCCCTCCCGGGTCCCGGGCCAGCCC	120						
Db	61	CGGCTCTCTCCGGCGGACCCCGCCCCGTCGCGACCCCTCCCGGGTCCCGGGCCAGCCC	120						
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Db	121	CTTCGGGGCCCTCCAGCCCTCCCTCTCTTTCGCGGGCCCGGCCCTCTCTCTCGGGCG	180						
QY	181	CGAGTTTCAGGAGCGCTGCGTCTGTCGCACTGGGAAGCCCTGGCCCCCGGCCACCC	240						

Db	181	CGAGTTTCAGGACGCTCGTCTCTGTCGACAGTGGAGAGCCCTGGCGCCCGGCCACCC	240
Qy	241	CCGCG 245	
Db	241	CCGCG 245	
RESULT 2			
AR455896			
LOCUS	AR455896	261 bp	DNA
DEFINITION	Sequence 24 from patent US 6686159.		
ACCESSION	AR455896		
VERSION	AR455896.1	GI:42690788	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 261)		
AUTHORS	Andrews,W.H., Foster,C.A., Frazer,S. and Mohammadpour,H.		
TITLE	Methods and compositions for modulating telomerase reverse		
JOURNAL	transcriptase (TERT) expression		
FEATURES	Patent: US 6686159-A 24 03-FEB-2004;		
source	Location/Qualifiers		
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Best Local Similarity	100.0%;	Pred. No. 4.7e-29;	
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Db	14	CCCCACGTGGCGGAGGACTGGGGACCCCGGACACCGTCTCTGCGCCCTTCCAGCT	73
Qy	61	CCGCTCTCTCCGCGGACCCCGCGTCCGACCCCTCCCGGGTCCCGGCCACAGCCC	120
Db	74	CCGCTCTCTCCGCGGACCCCGCGTCCGACCCCTCCCGGGTCCCGGCCACAGCCC	133
Qy	121	CTTCGGGGCCCTCCAGCCCTCCCTCTCTTCGCGGCGCCCGCCCTCTCTCGGGG	180
Db	134	CTTCGGGGCCCTCCAGCCCTCCCTCTCTTCGCGGCGCCCGCCCTCTCTCGGGG	193
Qy	181	CGAGTTTCAGGACGCTCGTCTGTCGCGACGTGGAGAGCCCTGGCCCGGCCACCC	240
Db	194	CGAGTTTCAGGACGCTCGTCTGTCGCGACGTGGAGAGCCCTGGCCCGGCCACCC	253
Qy	241	CCGCG 245	
Db	254	CCGCG 258	
RESULT 3			
AX817781/c			
LOCUS	AX817781	955 bp	DNA
DEFINITION	Sequence 17 from Patent WO02067861.		
ACCESSION	AX817781		
VERSION	AX817781.1	GI:39722976	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Oncolytic adenoviral vectors		
TITLE	Patent: WO 02067861-A 17 06-SEP-2002;		
JOURNAL	Location/Qualifiers		
FEATURES	1..955		
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Db	500	CCCCACGTGGCGGAGGACTGGGGACCCCGGACACCGTCTCTGCGCCCTTCCAGCT	441
Qy	61	CCGCTCTCTCCGCGGACCCCGCGTCCGACCCCTCCCGGGTCCCGGCCACAGCCC	120
Db	440	CCGCTCTCTCCGCGGACCCCGCGTCCGACCCCTCCCGGGTCCCGGCCACAGCCC	381
Qy	121	CCTCGGGCCCTCCAGCCCTCCCTCTCTTCGCGGCGCCCGCCCTCTCTCGGGG	180
Db	380	CCTCGGGCCCTCCAGCCCTCCCTCTCTTCGCGGCGCCCGCCCTCTCTCGGGG	321
Qy	181	CGAGTTTCAGGACGCTCGTCTGTCGCGACGTGGAGAGCCCTGGCCCGGCCACCC	240
Db	320	CGAGTTTCAGGACGCTCGTCTGTCGCGACGTGGAGAGCCCTGGCCCGGCCACCC	261
Qy	241	CCGCG 245	
Db	260	CCGCG 256	
RESULT 4			
AX003120			
LOCUS	AX003120	5126 bp	DNA
DEFINITION	Sequence 1 from Patent WO9933998		
ACCESSION	AX003120		
VERSION	AX003120.1	GI:9926982	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Wick, M. and Hagen, G.		
TITLE	Regulatory dna sequences of the human catalytic telomerase sub-unit		
JOURNAL	gene, diagnostic and therapeutic use thereof		
FEATURES	Patent: WO 9933998-A 1 08-JUL-1999;		
source	WICK MARESA (DE); BAYER AG (DE)		
	Location/Qualifiers		
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Query Match	100.0%;	Score 245;	DB 6; Length 5126;
Best Local Similarity	100.0%;	Pred. No. 1.6e-29;	
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Qy	61	CCGCTCTCTCCGCGGACCCCGCGTCCGACCCCTCCCGGGTCCCGGCCACAGCCC	120
Db	4939	CCGCTCTCTCCGCGGACCCCGCGTCCGACCCCTCCCGGGTCCCGGCCACAGCCC	4998
Qy	121	CCTCGGGCCCTCCAGCCCTCCCTCTCTTCGCGGCGCCCGCCCTCTCTCGGGG	180
Db	4999	CCTCGGGCCCTCCAGCCCTCCCTCTCTTCGCGGCGCCCGCCCTCTCTCGGGG	5058
Qy	181	CGAGTTTCAGGACGCTCGTCTGTCGCGACGTGGAGAGCCCTGGCCCGGCCACCC	240
Db	5059	CGAGTTTCAGGACGCTCGTCTGTCGCGACGTGGAGAGCCCTGGCCCGGCCACCC	5118

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QY      241  CCGCG 245
Db      5119  CCGCG 5123

RESULT 5
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LOCUS   Homo sapiens gene for telomerase transcriptase, partial cds.
DEFINITION
ACCESSION AB016767.1 GI:4239869
VERSION   AB016767.1
KEYWORDS telomerase transcriptase; hTERT.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE
AUTHORS   Takakura,M., Kyo,S., Kanaya,T., Hirano,H., Takeda,J., Yutsudo,M.
and Inoue,M.
TITLE     Cloning of human telomerase catalytic subunit (hTERT) gene promoter
and identification of proximal core promoter sequences essential
for transcriptional activation in immortalized and cancer cells
Cancer Res. 59 (3), 551-557 (1999)
JOURNAL   99137484
MEDLINE   9973199
REFERENCE
PUBMED    2 (bases 1 to 5491)
AUTHORS   Takakura,M., Kyo,S., Kanaya,T., Takeda,J. and Inoue,M.
TITLE     Direct Submision
JOURNAL   Submitted (04-AUG-1998) Masahiro Takakura, Kanazawa University,
School of Medicine, Department of Obstetrics and Gynecology; 13-1,
Takarumachi, Kanazawa, Ishikawa 920-0934, Japan
(E-mail: takakura@med.kanazawa-u.ac.jp. Tel:81-76-265-2425,
Fax:81-76-234-4266)
FEATURES             Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.6e-29; Indels 0; Gaps 0;
Matches 245; Conservative 0; Mismatches 0;

QY      1  CCCACAGTGGCGGAGGAGTGGGACCCGGGACCCGGGACCCGCTCTGCCCCCTTACCTTCCAGCT 60
Db      3170  CCCACAGTGGCGGAGGAGTGGGACCCGGGACCCGGGACCCGCTCTGCCCCCTTACCTTCCAGCT 3229

QY      61  CCGCTCTCTCCGCGGAGACCCCGCCCGCTTCCGACCCCTCCCGGGTCCCGGCCAGCCCC 120
Db      3230  CCGCTCTCTCCGCGGAGACCCCGCCCGCTTCCGACCCCTCCCGGGTCCCGGCCAGCCCC 3289

QY      121  CCTCGGGCCCTCCAGCCCTCCCTTCTTCCGGGGCCCGCCCTCTCTCTCGGGCG 180
Db      3290  CCTCGGGCCCTCCAGCCCTCCCTTCTTCCGGGGCCCGCCCTCTCTCTCGGGCG 3349

QY      181  CGAGTTTCAGGACAGCGCTGCGTCTGTCGACAGTGGGAAAGCCCTGGCCCGGCACCC 240
Db      3350  CGAGTTTCAGGACAGCGCTGCGTCTGTCGACAGTGGGAAAGCCCTGGCCCGGCACCC 3409

QY      241  CCGCG 245
Db      3410  CCGCG 3414

RESULT 6
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LOCUS   Sequence 25 from patent US 6686159.
DEFINITION
ACCESSION AR455897
VERSION   AR455897.1 GI:42690789
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 5928)
AUTHORS   Andrews,W.H., Foster,C.A., Fraser,S. and Mohammadpour,H.
TITLE     Methods and compositions for modulating telomerase reverse
transcriptase (TERT) expression
JOURNAL   Patent: US 6686159-A 25 03-FEB-2004;
FEATURES             Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      51  CCCACAGTGGCGGAGGAGTGGGACCCGGGACCCGGGACCCGCTCTGCCCCCTTACCTTCCAGCT 110

QY      61  CCGCTCTCTCCGCGGAGACCCCGCCCGCTTCCGACCCCTCCGGGTCCCGGCCAGCCCC 120
Db      111  CCGCTCTCTCCGCGGAGACCCCGCCCGCTTCCGACCCCTCCGGGTCCCGGCCAGCCCC 170

QY      121  CCTCGGGCCCTCCAGCCCTCCCTTCTTTCGGGGCCCGCCCTCTCTCTCGGGCG 180
Db      171  CCTCGGGCCCTCCAGCCCTCCCTTCTTTCGGGGCCCGCCCTCTCTCTCGGGCG 230

QY      181  CGAGTTTCAGGACAGCGCTGCGTCTGTCGACAGTGGGAAAGCCCTGGCCCGGCACCC 240
Db      231  CGAGTTTCAGGACAGCGCTGCGTCTGTCGACAGTGGGAAAGCCCTGGCCCGGCACCC 290

QY      241  CCGCG 245
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Db 291 CCGCG 295

RESULT 7
LOCUS AX003122 11276 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 3 from Patent WO9933998.
ACCESSION AX003122
VERSION AX003122.1 GI:9926984
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Wick, M., and Hagen, G.
TITLE Regulatory dna sequences of the human catalytic telomerase sub-unit
gene, diagnostic and therapeutic use thereof
JOURNAL WICK MARESA (DE); BAYER AG (DE)
PATENT: WO 9933998-A 3 08-JUL-1999;
FEATURES
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2e-29;
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Db 11089 CGCCTCTCTCGCGGAGGACCCGCGGTCCTGACCCCTCCGGGTCCTGCGGCGGCGG 11148
Qy 121 CTTCCGGGCGCTCCAGCCCTCCCTCTCTTTCGGGCGGCGGCGGCTCTCTCGGGGGG 180
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Qy 181 CGAGTTTCAGGACGCGTGCGTCTGCTGCGACGTTGGGAAGCCCTGGCGCCCGGCGCACCC 240
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Qy 241 CCGCG 245
Db 11269 CCGCG 11273

RESULT 8
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LOCUS HSTERT1 26414 bp DNA linear PRI 13-MAY-1999
DEFINITION Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6.
ACCESSION AF128893
VERSION AF128893.1 GI:4808970
KEYWORDS
SEGMENT 1 of 2
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 26414)
AUTHORS Wick, M., Zubov, D. and Hagen, G.
TITLE Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT)
JOURNAL Gene 232 (1), 97-106 (1999)
MEDLINE 99267414
PUBMED 10333526
REFERENCE 2 (bases 1 to 26414)

Wick, M., Zubov, D. and Hagen, G.
Direct Submission
Submitted (16-FEB-1999) Dept. of Mol. Biol., Bayer AG Leverkusen,
ZF-BTM, Bldg. Q18, Leverkusen D-51368, Germany

FEATURES
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Qy 1 CCCACGTGCGGAGGAGCTGGGGACCCGGGACCCGTCCTGCCCCCTTACCTTCCAGCT 60
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Qy 241 CCGCG 245
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RESULT 9
AR266023
LOCUS AR266023 51552 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 30 from patent US 6492171.
ACCESSION AR266023
VERSION AR266023.1 GI:29694869
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51552)
AUTHORS Monia, B.P., Gaarde, W.A., Freier, S.M. and Wanciewicz, E.
TITLE Antisense modulation of TERT expression
JOURNAL Patent: US 6492171-A 30 10-DEC-2002;
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DEFINITION Sequence 6 from patent US 6610839.
ACCESSION AR390473
VERSION AR390473.1 GI:40112397
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 4321)
AUTHORS Morin,G.B. and Andrews,W.H.
TITLE Promoter for telomerase reverse transcriptase
JOURNAL Patent: US 6610839-A 6 26-AUG-2003;
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source Location/Qualifiers
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QY 242 CGCG 245
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Db 2479 CGCG 2482

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LOCUS AF097365 4356 bp DNA linear PRI 02-FEB-1999
DEFINITION Homo sapiens telomerase reverse transcriptase (TERT) gene, promoter
and partial cds.
ACCESSION AF097365
VERSION AF097365.1 GI:4210970
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 4356)
AUTHORS Cong,Y.S., Wen,J. and Bacchetti,S.
TITLE The human telomerase catalytic subunit hTERT: organization of the
gene and characterization of the promoter
JOURNAL Hum. Mol. Genet. 8 (1), 137-142 (1999)
MEDLINE 99105927
PUBMED 9887342
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REFERENCE
2 (bases 1 to 4356)
AUTHORS Cong,Y.S., Wen,J. and Bacchetti,S.
TITLE Direct Submission
JOURNAL Submitted (05-OCT-1998) Pathology, McMaster University, 1200 Main
St. W., Hamilton, ON L8N 3Z5, Canada
FEATURES
source Location/Qualifiers
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Db 3993 CGCG 3996

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cds.
ACCESSION AF121948
VERSION AF121948.1 GI:4580662
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 15332)
AUTHORS Greenberg,R.A., O'Hagan,R.C., Deng,H., Xiao,Q., Hann,S.R.,
Adams,R.R., Lichtsteiner,S., Chin,L., Morin,G.B. and DePinho,R.A.
TITLE Telomerase reverse transcriptase gene is a direct target of c-Myc
but is not functionally equivalent in cellular transformation
JOURNAL Oncogene 18 (5), 1219-1226 (1999)
MEDLINE 99144726
PUBMED 10022128
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REFERENCE 2 (bases 1 to 15332)
AUTHORS Morin,G.B., Carlos,R. and Adams,R.R.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-1999) Geron Corporation, 230 Constitution Drive,
Menlo Park, CA 94025, USA
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JOURNAL Patent: US 6576464-A 1 10-JUN-2003;
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Qy 182 GAGTTTCAGGCAGCGCTGCGTCTGCGGACGCTGGGAAGCCCTGGCCCGGCCACCCCC 241
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Job time : 1230.58 secs

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LOCUS AR342806 15418 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6576464.
ACCESSION AR342806
VERSION AR342806.1 GI:33738009
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Gold,J.D. and Lebkowski,J.S.
TITLE Methods for providing differentiated stem cells

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-10-081-969-94

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Searched: 5615251 seqs, 3030001701 residues

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4	245	100.0	261	19	US-10-863-075-24
5	245	100.0	295	15	US-10-140-763A-12
6	245	100.0	955	15	US-10-081-969-17
7	245	100.0	5126	19	US-10-840-455-1
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					Sequence 24, Appl
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16	244	99.6	397	15	US-10-081-969-93	Sequence 93, Appl
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19	244	99.6	4321	17	US-10-325-810-6	Sequence 6, Appl
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23	244	99.6	15418	14	US-10-141-220-1	Sequence 1, Appl
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26	244	99.6	15418	17	US-10-674-836-1	Sequence 1, Appl
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32	229	93.5	361	18	US-10-456-830-8	Sequence 8, Appl
33	229	93.5	381	18	US-10-456-830-9	Sequence 9, Appl
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37	201.2	82.1	35871	9	US-09-956-335-2	Sequence 2, Appl
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43	198	80.8	1677	9	US-09-956-335-3	Sequence 3, Appl
44	183.2	74.8	4356	17	US-10-240-589C-144	Sequence 144, App
45	144	58.8	144	15	US-10-219-450-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-10-081-969-94

; Sequence 94, Application US/10081969

; Publication No. US20030104625A1

; GENERAL INFORMATION:

; APPLICANT: Cheng, Cheng

; APPLICANT: Clarke, Lori

; APPLICANT: Connelly, Sheila

; APPLICANT: Ennist, David

; APPLICANT: Forry-Schaudies, Suzanne

; APPLICANT: Gorziglia, Mario

; APPLICANT: Hallenbeck, Paul

; APPLICANT: Hay, Carl

; APPLICANT: Jakubczak, John

; APPLICANT: Kaleko, Michael

; APPLICANT: Phipps, Sandrina

; APPLICANT: Police, Seshidhar

; APPLICANT: Ryan, Patricia

; APPLICANT: Steward, David

; APPLICANT: Xie, Yuefeng

; TITLE OF INVENTION: No. US20030104625A1el Oncolytic Adenoviral Vectors

; FILE REFERENCE: 4-31704A/GTI

; CURRENT APPLICATION NUMBER: US/10/081,969

; CURRENT FILING DATE: 2002-02-22

; PRIOR APPLICATION NUMBER: US 60/270,922

; PRIOR FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: US 60/295,037

; PRIOR FILING DATE: 2001-06-01

; PRIOR APPLICATION NUMBER: US 60/348,670

; PRIOR FILING DATE: 2000-01-14

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 94

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TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(245)
OTHER INFORMATION: A 245 bp fragment of the hTERT promoter
US-10-081-969-94

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Best Local Similarity 100.0%; Pred. No. 7.1e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCAGTGGCGAGGAGTGGGGACCCCGGACCCCGTCTCTCCGCGCCCGCCCTTCCAGCT 60
DB 1 CCCCAGTGGCGAGGAGTGGGGACCCCGGACCCCGTCTCTCCGCGCCCGCCCTTCCAGCT 60

QY 61 CGGCTCTCTCCGCGCGGAGACCCCGCCCGTCCGACCCCTCCCGGGTCCCGGCCAGGCC 120
DB 61 CGGCTCTCTCCGCGCGGAGACCCCGCCCGTCCGACCCCTCCCGGGTCCCGGCCAGGCC 120

QY 121 CTTCCGGGCTCCCGACCCCTCCCTTCTTCCGCGCCCGCCCTCTCTCCGCGG 180
DB 121 CTTCCGGGCTCCCGACCCCTCCCTTCTTCCGCGCCCGCCCTCTCTCCGCGG 180

QY 181 CGAGTTTCAGGAGCGCTGCTCTCTGCGCACGTGGGAAGCCCTGGCCCGGCCACCC 240
DB 181 CGAGTTTCAGGAGCGCTGCTCTCTGCGCACGTGGGAAGCCCTGGCCCGGCCACCC 240

QY 241 CCGCG 245
DB 241 CCGCG 245

RESULT 2

US-09-932-581-24
Sequence 24, Application US/09932581
Publication No. US20030050264A1
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Foster, Christopher A.
APPLICANT: Fraser, Stephanie
APPLICANT: Mohammadpour, Hamid
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REFERENCE: SIER-005
CURRENT APPLICATION NUMBER: US/09/932,581
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/227,865
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/238,345
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 261
TYPE: DNA
ORGANISM: human
US-09-932-581-24

Query Match 100.0%; Score 245; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 7.1e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCAGTGGCGAGGAGTGGGGACCCCGGACCCCGTCTCTCCGCGCCCGCCCTTCCAGCT 60
DB 14 CCCCAGTGGCGAGGAGTGGGGACCCCGGACCCCGTCTCTCCGCGCCCGCCCTTCCAGCT 73

QY 61 CGGCTCTCTCCGCGCGGAGACCCCGCCCGTCCGACCCCTCCCGGGTCCCGGCCAGGCC 120
DB 74 CGGCTCTCTCCGCGCGGAGACCCCGCCCGTCCGACCCCTCCCGGGTCCCGGCCAGGCC 133

QY 121 CTTCCGGGCTCCCGACCCCTCCCTTCTTCCGCGCCCGCCCTTCTCTCCGCGG 180
DB 134 CTTCCGGGCTCCCGACCCCTCCCTTCTTCCGCGCCCGCCCTTCTCTCCGCGG 193

QY 181 CGAGTTTCAGGAGCGCTGCTCTCTGCGCACGTGGGAAGCCCTGGCCCGGCCACCC 240
DB 194 CGAGTTTCAGGAGCGCTGCTCTCTGCGCACGTGGGAAGCCCTGGCCCGGCCACCC 253

QY 241 CCGCG 245
DB 254 CCGCG 258

RESULT 3

US-10-338-294-24
Sequence 24, Application US/10338294
Publication No. US20030171326A1
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Foster, Christopher A.
APPLICANT: Fraser, Stephanie
APPLICANT: Mohammadpour, Hamid
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REFERENCE: SIER-005
CURRENT APPLICATION NUMBER: US/10/338,294
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US/09/932,581
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/227,865
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/238,345
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 261
TYPE: DNA
ORGANISM: human
US-10-338-294-24

Query Match 100.0%; Score 245; DB 16; Length 261;
Best Local Similarity 100.0%; Pred. No. 7.1e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCAGTGGCGAGGAGTGGGGACCCCGGACCCCGTCTCTCCGCGCCCGCCCTTCCAGCT 60
DB 14 CCCCAGTGGCGAGGAGTGGGGACCCCGGACCCCGTCTCTCCGCGCCCGCCCTTCCAGCT 73

QY 61 CGGCTCTCTCCGCGCGGAGACCCCGCCCGTCCCGACCCCTTCCCGGGTCCCGGCCAGGCC 120
DB 74 CGGCTCTCTCCGCGCGGAGACCCCGCCCGTCCCGACCCCTTCCCGGGTCCCGGCCAGGCC 133

QY 121 CTTCCGGGCTCCCGACCCCTTCCCTTCTTCCGCGCCCGCCCTTCTCTCCGCGG 180
DB 134 CTTCCGGGCTCCCGACCCCTTCCCTTCTTCCGCGCCCGCCCTTCTCTCCGCGG 193

QY 181 CGAGTTTCAGGAGCGCTGCTCTGCGCACGTGGGAAGCCCTGGCCCGGCCACCC 240
DB 194 CGAGTTTCAGGAGCGCTGCTCTGCGCACGTGGGAAGCCCTGGCCCGGCCACCC 253

QY 241 CCGCG 245
DB 254 CCGCG 258

RESULT 4

US-10-863-075-24
Sequence 24, Application US/10863075
Publication No. US2005005962A1
GENERAL INFORMATION:

APPLICANT: Andrews, William H.
APPLICANT: Foster, Christopher A.
APPLICANT: Fraser, Stephanie
APPLICANT: Mohammadpour, Hamid
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REFERENCE: SIER-005
CURRENT APPLICATION NUMBER: US/10/863,075
CURRENT FILING DATE: 2004-06-07
PRIOR APPLICATION NUMBER: 60/227,865
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/238,345
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 261
TYPE: DNA
ORGANISM: human
US-10-863-075-24

Query Match 100.0%; Score 245; DB 19; Length 261;
Best Local Similarity 100.0%; Pred. No. 7.1e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCACAGTGGCGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCCTTCCAGCT 60
Db 14 CCCACAGTGGCGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 73
Qy 61 CCGCTCTCTCCGCGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 120
Db 74 CCGCTCTCTCCGCGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 133
Qy 121 CCGCTCTCTCCGCGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 180
Db 134 CCGCTCTCTCCGCGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 193
Qy 181 CGAGTTTCAGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 240
Db 194 CGAGTTTCAGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 253
Qy 241 CCGCG 245
Db 254 CCGCG 258

RESULT 5
US-10-140-763A-12
Sequence 12, Application US/10140763A
Publication No. US20030104420A1
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Methods and Compositions for Modulating
Telomerase Reverse Transcriptase (TERT) Expression
FILE REFERENCE: SIER-012
CURRENT APPLICATION NUMBER: US/10/140,763A
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/289,641
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 295
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide
US-10-140-763A-12

Query Match 100.0%; Score 245; DB 15; Length 295;
Best Local Similarity 100.0%; Pred. No. 6.9e-51;

Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCACAGTGGCGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 60
Db 36 CCCACAGTGGCGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 95
Qy 61 CCGCTCTCTCCGCGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 120
Db 96 CCGCTCTCTCCGCGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 155
Qy 121 CCGCTCTCTCCGCGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 180
Db 156 CCGCTCTCTCCGCGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 215
Qy 181 CGAGTTTCAGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 240
Db 216 CGAGTTTCAGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 275
Qy 241 CCGCG 245
Db 276 CCGCG 280

RESULT 6
US-10-081-969-17/c
Sequence 17, Application US/10081969
Publication No. US20030104625A1
GENERAL INFORMATION:
APPLICANT: Cheng, Cheng
APPLICANT: Clarke, Lori
APPLICANT: Connelly, Sheila
APPLICANT: Ennist, David
APPLICANT: Forzy-Schaudies, Suzanne
APPLICANT: Gorziglia, Mario
APPLICANT: Hallenbeck, Paul
APPLICANT: Hay, Carl
APPLICANT: Jakubczak, John
APPLICANT: Kaleko, Michael
APPLICANT: Phipps, Sandrina
APPLICANT: Police, Seshidhar
APPLICANT: Ryan, Patricia
APPLICANT: Steward, David
APPLICANT: Xie, Yuefeng
TITLE OF INVENTION: No. US20030104625A1el Oncolytic Adenoviral Vectors
FILE REFERENCE: 4-31704A/GTI
CURRENT APPLICATION NUMBER: US/10/081,969
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/270,922
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/295,037
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/348,670
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 955
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Viral vector sequence
NAME/KEY: misc feature
LOCATION: (1)-(955)
OTHER INFORMATION: Fig.47. Sequence of the right end of Arl7pAE2FTtex
US-10-081-969-17

Query Match 100.0%; Score 245; DB 15; Length 955;
Best Local Similarity 100.0%; Pred. No. 4.9e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACAGTGGCGGAGGAGTGGGACCCGGGACCCGCTCTCCCTTCCAGCT 60

Db 500 CCCACGTGGCGGAGGAGTGGGAGACCCGGGACACCGTCTCTGCCCTTACCTTCCAGCT 441
Qy 61 CCGCTCTCTCGCGCGGAGACCCCGCCCGTCTCCGACCCCTCCCGGGTCCCGGGCCAGCCC 120
Db 440 CCGCTCTCTCGCGCGGAGACCCCGCCCGTCTCCGACCCCTCCCGGGTCCCGGGCCAGCCC 381
Qy 121 CCTCGGGCCCTCCAGCCCTCTCCCTTCTTTCGCGGGCCCGCCCTCTCTCTCGGGCG 180
Db 380 CCTCGGGCCCTCCAGCCCTCTCCCTTCTTTCGCGGGCCCGCCCTCTCTCTCGGGCG 321
Qy 181 CGAGTTTCAGGACGCTGCTGCTGCTGCGCAGTGGGAGCCCTGGCCCGGCCACCC 240
Db 320 CGAGTTTCAGGACGCTGCTGCTGCTGCGCAGTGGGAGCCCTGGCCCGGCCACCC 261
Qy 241 CCGCG 245
Db 260 CCGCG 256
RESULT 7
US-10-840-455-1
; Sequence 1, Application US/10840455
; Publication No. US2005032094A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hegen, Gustav
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
; FILE REFERENCE: Lea 32 805C1
; CURRENT APPLICATION NUMBER: US/10/840,455
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: PCT/EP98/08216
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/582,246
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: DE19757984.1
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 5126
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-455-1
Query Match 100.0%; Score 245; DB 19; Length 5126;
Best Local Similarity 100.0%; Pred. No. 3.1e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACGTGGCGGAGGAGTGGGAGACCCGGGACCCCGTCTCTGCCCTTACCTTCCAGCT 60
Db 4879 CCCACGTGGCGGAGGAGTGGGAGACCCGGGACCCCGTCTCTGCCCTTACCTTCCAGCT 4938
Qy 61 CCGCTCTCTCGCGCGGAGACCCCGCCCGTCTCCGACCCCTCCCGGGTCCCGGGCCAGCCC 120
Db 4939 CCGCTCTCTCGCGCGGAGACCCCGCCCGTCTCCGACCCCTCCCGGGTCCCGGGCCAGCCC 4998
Qy 121 CTTCCGGGCTCTCCAGCCCTCTCCCTTCTTTCGCGGGCCCGCCCTCTCTCTCGGGCG 180
Db 4999 CTTCCGGGCTCTCCAGCCCTCTCCCTTCTTTCGCGGGCCCGCCCTCTCTCTCGGGCG 5058
Qy 181 CGAGTTTCAGGACGCTGCTGCTGCTGCGCAGTGGGAGCCCTGGCCCGGCCACCC 240
Db 5059 CGAGTTTCAGGACGCTGCTGCTGCTGCGCAGTGGGAGCCCTGGCCCGGCCACCC 5118
Qy 241 CCGCG 245
Db 5119 CCGCG 5123

RESULT 8

US-09-932-581-25
; Sequence 25, Application US/09932581
; Publication No. US20030050264A1
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Foster, Christopher A.
; APPLICANT: Fraser, Stephanie
; APPLICANT: Mohammadpour, Hamid
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
; FILE REFERENCE: SIER-005
; CURRENT APPLICATION NUMBER: US/09/932,581
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/227,865
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/230,174
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/238,345
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 5928
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic expression plasmid
US-09-932-581-25
Query Match 100.0%; Score 245; DB 10; Length 5928;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACGTGGCGGAGGAGTGGGAGACCCGGGACCCCGTCTCTGCCCTTACCTTCCAGCT 60
Db 51 CCCACGTGGCGGAGGAGTGGGAGACCCGGGACCCCGTCTCTGCCCTTACCTTCCAGCT 110
Qy 61 CCGCTCTCTCGCGCGGAGACCCCGCCCGTCTCCGACCCCTCCCGGGTCCCGGGCCAGCCC 120
Db 111 CCGCTCTCTCGCGCGGAGACCCCGCCCGTCTCCGACCCCTCCCGGGTCCCGGGCCAGCCC 170
Qy 121 CTTCCGGGCTCTCCAGCCCTCTCCCTTCTTTCGCGGGCCCGCCCTCTCTCTCGGGCG 180
Db 171 CTTCCGGGCTCTCCAGCCCTCTCCCTTCTTTCGCGGGCCCGCCCTCTCTCTCGGGCG 230
Qy 181 CGAGTTTCAGGACGCTGCTGCTGCTGCGCAGTGGGAGCCCTGGCCCGGCCACCC 240
Db 231 CGAGTTTCAGGACGCTGCTGCTGCTGCGCAGTGGGAGCCCTGGCCCGGCCACCC 290
Qy 241 CCGCG 245
Db 291 CCGCG 295

RESULT 9
US-10-338-294-25
; Sequence 25, Application US/10338294
; Publication No. US20030171326A1
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Foster, Christopher A.
; APPLICANT: Fraser, Stephanie
; APPLICANT: Mohammadpour, Hamid
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
; FILE REFERENCE: SIER-005
; CURRENT APPLICATION NUMBER: US/10/338,294
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US/09/932,581
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/227,865
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/230,174

```
/ PRIOR FILING DATE: 2000-09-01
/ PRIOR APPLICATION NUMBER: 60/238,345
/ PRIOR FILING DATE: 2000-10-05
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 25
/ LENGTH: 5928
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic expression plasmid
US-10-338-294-25

Query Match      100.0%; Score 245; DB 16; Length 5928;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACAGTGGCGGAGGAGTGGGGACCGGGACCGCTGCGCCCTTACCTTCCAGCT 60
DB 51 CCCACAGTGGCGGAGGAGTGGGGACCGGGACCGCTGCGCCCTTACCTTCCAGCT 110
QY 61 CCGCTCTCTCCGCGCGGACCGCGCCCTTCCCGACCCCTTCCGGGTCCCGGCCAGGCC 120
DB 111 CCGCTCTCTCCGCGCGGACCGCGCCCTTCCCGACCCCTTCCGGGTCCCGGCCAGGCC 170
QY 121 CCGCTCTCTCCGCGCGGACCGCGCCCTTCCCGACCCCTTCCGGGTCCCGGCCAGGCC 180
DB 171 CCGCTCTCTCCGCGCGGACCGCGCCCTTCCCGACCCCTTCCGGGTCCCGGCCAGGCC 230
QY 181 CGAGTTTCAGGACGCGTGGTCTGCTGCGACGCTGGGAGAGCCCTTGGCCCGGCCACCC 240
DB 231 CGAGTTTCAGGACGCGTGGTCTGCTGCGACGCTGGGAGAGCCCTTGGCCCGGCCACCC 290
QY 241 CCGCG 245
DB 291 CCGCG 295

RESULT 10
US-10-863-075-25
/ Sequence 25, Application US/10863075
/ Publication No. US20050059622A1
/ GENERAL INFORMATION:
/ APPLICANT: Andrews, William H.
/ APPLICANT: Foster, Christopher A.
/ APPLICANT: Fraser, Stephanie
/ APPLICANT: Mohammadpour, Hamid
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
/ TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
/ FILE REFERENCE: SIER-005
/ CURRENT APPLICATION NUMBER: US/10/863,075
/ CURRENT FILING DATE: 2004-06-07
/ PRIOR APPLICATION NUMBER: 60/227,865
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: 60/230,174
/ PRIOR FILING DATE: 2000-09-01
/ PRIOR APPLICATION NUMBER: 60/238,345
/ PRIOR FILING DATE: 2000-10-05
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 25
/ LENGTH: 5928
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic expression plasmid
US-10-863-075-25

Query Match      100.0%; Score 245; DB 19; Length 5928;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACAGTGGCGGAGGAGTGGGGACCGGGACCGCTGCGCCCTTACCTTCCAGCT 60
```

```
DB 51 CCCACAGTGGCGGAGGAGTGGGGACCGGGACCGCTGCGCCCTTACCTTCCAGCT 110
QY 61 CCGCTCTCTCCGCGCGGACCGCGCCCTTCCCGACCCCTTCCGGGTCCCGGCCAGGCC 120
DB 111 CCGCTCTCTCCGCGCGGACCGCGCCCTTCCCGACCCCTTCCGGGTCCCGGCCAGGCC 170
QY 121 CCGCTCTCTCCGCGCGGACCGCGCCCTTCCCGACCCCTTCCGGGTCCCGGCCAGGCC 180
DB 171 CCGCTCTCTCCGCGCGGACCGCGCCCTTCCCGACCCCTTCCGGGTCCCGGCCAGGCC 230
QY 181 CGAGTTTCAGGACGCGTGGTCTGCTGCGACGCTGGGAGAGCCCTTGGCCCGGCCACCC 240
DB 231 CGAGTTTCAGGACGCGTGGTCTGCTGCGACGCTGGGAGAGCCCTTGGCCCGGCCACCC 290
QY 241 CCGCG 245
DB 291 CCGCG 295

RESULT 11
US-10-840-455-3
/ Sequence 3, Application US/10840455
/ Publication No. US20050032094A1
/ GENERAL INFORMATION:
/ APPLICANT: Bayer Aktiengesellschaft
/ APPLICANT: Hagen, Gustav
/ APPLICANT: Wick, Mareisa
/ APPLICANT: Zubov, Dmitry
/ TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
/ TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
/ FILE REFERENCE: Lea 32 805C1
/ CURRENT APPLICATION NUMBER: US/10/840,455
/ CURRENT FILING DATE: 2004-05-06
/ PRIOR APPLICATION NUMBER: PCT/EP98/08216
/ PRIOR FILING DATE: 1998-12-22
/ PRIOR APPLICATION NUMBER: US 09/582,246
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: DE19757984.1
/ PRIOR FILING DATE: 1997-12-24
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 3
/ LENGTH: 11276
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-840-455-3

Query Match      100.0%; Score 245; DB 19; Length 11276;
Best Local Similarity 100.0%; Pred. No. 2.5e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACAGTGGCGGAGGAGTGGGGACCGGGACCGCTGCGCCCTTACCTTCCAGCT 60
DB 11029 CCCACAGTGGCGGAGGAGTGGGGACCGGGACCGCTGCGCCCTTACCTTCCAGCT 11088
QY 61 CCGCTCTCTCCGCGCGGACCGCGCCCTTCCCGACCCCTTCCGGGTCCCGGCCAGGCC 120
DB 11089 CCGCTCTCTCCGCGCGGACCGCGCCCTTCCCGACCCCTTCCGGGTCCCGGCCAGGCC 11148
QY 121 CCGCTCTCTCCGCGCGGACCGCGCCCTTCCCGACCCCTTCCGGGTCCCGGCCAGGCC 180
DB 11149 CCGCTCTCTCCGCGCGGACCGCGCCCTTCCCGACCCCTTCCGGGTCCCGGCCAGGCC 11208
QY 181 CGAGTTTCAGGACGCGTGGTCTGCTGCGACGCTGGGAGAGCCCTTGGCCCGGCCACCC 240
DB 11209 CGAGTTTCAGGACGCGTGGTCTGCTGCGACGCTGGGAGAGCCCTTGGCCCGGCCACCC 11268
QY 241 CCGCG 245
DB 11269 CCGCG 11273
```

RESULT 12

US-10-840-455-43
; Sequence 43, Application US/10840455
; Publication No. US20050032094A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hegen, Gustav
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
; FILE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
; FILE REFERENCE: Lea 32 805C1
; CURRENT APPLICATION NUMBER: US/10/840,455
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: PCT/EP98/08216
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/582,246
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: DE19757984.1
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 26414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-455-43

Query Match 100.0%; Score 245; DB 19; Length 26414;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGCTGCGGAGGACTGGGGACCCGGGACCCCGCTCTGCCCCCTTACCTTCCAGCT 60
DB 11029 CCCACGCTGCGGAGGACTGGGGACCCGGGACCCCGCTCTGCCCCCTTACCTTCCAGCT 11088

QY 61 CCGCTCTCTCGGCGGACCCCGCCCGCTCCGACCCCTCCCGGGTCCCGGGCCACGCCC 120
DB 11089 CCGCTCTCTCGGCGGACCCCGCCCGCTCCGACCCCTCCCGGGTCCCGGGCCACGCCC 11148

QY 121 CTTCCGGGCTCCCGACGCTCCCTTCTTCCGCGGCGCCGCTCTCTCGGGGG 180
DB 11149 CTTCCGGGCTCCCGACGCTCCCTTCTTCCGCGGCGCCGCTCTCTCGGGGG 11208

QY 181 CGAGTTTACGACGCTCGCTCTCTGCGCAGTGGGAAGCCCTGGCCCGGCCACCC 240
DB 11209 CGAGTTTACGACGCTCGCTCTCTGCGCAGTGGGAAGCCCTGGCCCGGCCACCC 11268

QY 241 CCGCG 245
DB 11269 CCGCG 11273

RESULT 13

US-09-733-294A-30
; Sequence 30, Application US/09733294A
; Patent No. US20020045588A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 30
; LENGTH: 51552
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: exon
; LOCATION: (1)...(11492)
; OTHER INFORMATION: exon 1
; NAME/KEY: intron
; LOCATION: (11493)...(11596)
; OTHER INFORMATION: intron 1
; NAME/KEY: exon
; LOCATION: (11597)...(12950)
; OTHER INFORMATION: exon 2
; NAME/KEY: intron
; LOCATION: (12951)...(21566)
; OTHER INFORMATION: intron 2
; NAME/KEY: exon
; LOCATION: (21567)...(21762)
; OTHER INFORMATION: exon 3
; NAME/KEY: intron
; LOCATION: (21763)...(23851)
; OTHER INFORMATION: intron 3
; NAME/KEY: exon
; LOCATION: (23852)...(24032)
; OTHER INFORMATION: exon 4
; NAME/KEY: intron
; LOCATION: (24033)...(24719)
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; NAME/KEY: exon
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; OTHER INFORMATION: exon 5
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; OTHER INFORMATION: exon 6
; NAME/KEY: intron
; LOCATION: (25550)...(30196)
; OTHER INFORMATION: intron 6
; NAME/KEY: exon
; LOCATION: (30195)...(30292)
; OTHER INFORMATION: exon 7
; NAME/KEY: intron
; LOCATION: (30293)...(31272)
; OTHER INFORMATION: intron 7
; NAME/KEY: exon
; LOCATION: (31273)...(31358)
; OTHER INFORMATION: exon 8
; NAME/KEY: intron
; LOCATION: (31359)...(33843)
; OTHER INFORMATION: intron 8
; NAME/KEY: unsure
; LOCATION: 31450
; OTHER INFORMATION: unknown
; NAME/KEY: exon
; LOCATION: (33844)...(33957)
; OTHER INFORMATION: exon 9
; NAME/KEY: intron
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; OTHER INFORMATION: intron 9
; NAME/KEY: exon
; LOCATION: (35942)...(36013)
; OTHER INFORMATION: exon 10
; NAME/KEY: intron
; LOCATION: (36014)...(37884)
; OTHER INFORMATION: intron 10
; NAME/KEY: exon
; LOCATION: (37885)...(38073)
; OTHER INFORMATION: exon 11
; NAME/KEY: intron
; LOCATION: (38074)...(41874)
; OTHER INFORMATION: intron 11
; NAME/KEY: exon
; LOCATION: (41875)...(42001)
; OTHER INFORMATION: exon 12

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; NAME/KEY: intron
; LOCATION: (42002)...(42881)
; OTHER INFORMATION: intron 12
; NAME/KEY: exon
; LOCATION: (42882)...(42943)
; OTHER INFORMATION: exon 13
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; LOCATION: (42944)...(46129)
; OTHER INFORMATION: intron 13
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; LOCATION: (46130)...(46254)
; OTHER INFORMATION: exon 14
; NAME/KEY: intron
; LOCATION: (46255)...(47035)
; OTHER INFORMATION: intron 14
; NAME/KEY: exon
; LOCATION: (47036)...(47173)
; OTHER INFORMATION: exon 15
; NAME/KEY: intron
; LOCATION: (47174)...(47709)
; OTHER INFORMATION: intron 15
; NAME/KEY: exon
; LOCATION: (47710)...(50544)
; OTHER INFORMATION: exon 16
US-09-733-294A-30

Query Match          100.0%; Score 245; DB 9; Length 51552;
Best Local Similarity 100.0%; Pred. No. 1.6e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACAGTGGCGAGGAGCTGGGGACCCCGGGACCCCGTCTGCTGCTTCACTTCCAGCT 60
DB 11029 CCCACAGTGGCGAGGAGCTGGGGACCCCGGGACCCCGTCTGCTGCTTCACTTCCAGCT 11088

QY 61 CGCCTCTCTCGCGGGACCCCGCGCTCCCGACCCCTCCCGGGTCCCGGGCCCGAGCCC 120
DB 11089 CGCCTCTCTCGCGGGACCCCGCGCTCCCGACCCCTCCCGGGTCCCGGGCCCGAGCCC 11148

QY 121 CTCCGGGCGCTCCCGAGCCCTCCCTTCTTCCGGCGGCGCCGCGCTCTCTCGCGGG 180
DB 11149 CTCCGGGCGCTCCCGAGCCCTCCCTTCTTCCGGCGGCGCCGCGCTCTCTCGCGGG 11208

QY 181 CGAGTTTCAGGACGCTGCGTCTGCTGCGACCTTGGGAAGCCCTGGCCCGGCAACC 240
DB 11209 CGAGTTTCAGGACGCTGCGTCTGCTGCGACCTTGGGAAGCCCTGGCCCGGCAACC 11268

QY 241 CGCG 245
DB 11269 CGCG 11273

RESULT 14
US-10-674-836-17
; Sequence 17, Application US/10674836
; Publication No. US20040072787A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vassebot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/10/674,836
; CURRENT FILING DATE: 2003-09-29
; PRIOR FILING DATE: US/09/244,438
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 298
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-10-674-836-17

Query Match          99.6%; Score 244; DB 17; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCACGTGGCGAGGAGCTGGGGACCCCGGGACCCCGTCTGCTGCTTCACTTCCAGCTC 61
DB 52 CCCACGTGGCGAGGAGCTGGGGACCCCGGGACCCCGTCTGCTGCTTCACTTCCAGCTC 111

QY 62 CGCCTCTCTCGCGGGACCCCGCGCTCCCGACCCCTCCCGGGTCCCGGGCCCGAGCCC 121
DB 112 CGCCTCTCTCGCGGGACCCCGCGCTCCCGACCCCTCCCGGGTCCCGGGCCCGAGCCC 171

QY 122 CTCCGGGCGCTCCCGAGCCCTCCCTTCTTCCGGGCGGCGCCCTCTCTCGGGGGC 181
DB 172 CTCCGGGCGCTCCCGAGCCCTCCCTTCTTCCGGGCGGCGCCCTCTCTCGGGGGC 231

QY 182 GAGTTTCAGGACGCTGCGTCTGCTGCGACGCTGGGAAGCCCTGGCCCGGCAACC 241
DB 232 GAGTTTCAGGACGCTGCGTCTGCTGCGACGCTGGGAAGCCCTGGCCCGGCAACC 291

QY 242 CGCG 245
DB 292 CGCG 295

RESULT 15
US-10-212-667-1
; Sequence 1, Application US/10212667
; Publication No. US20030082722A1
; GENERAL INFORMATION:
; APPLICANT: FANG, BIANGLIANG
; TITLE OF INVENTION: METHOD FOR AMPLIFYING EXPRESSION FROM A CELL SPECIFIC
; FILE REFERENCE: UTSC:708US
; CURRENT APPLICATION NUMBER: US/10/212,667
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/310,905
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-212-667-1

Query Match          99.6%; Score 244; DB 14; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.1e-50;
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QY 1 CCCACAGTGGCGAGGAGCTGGGGACCCCGGGACCCCGTCTGCTGCTTCACTTCCAGCT 60
DB 135 CCCACAGTGGCGAGGAGCTGGGGACCCCGGGACCCCGTCTGCTGCTTCACTTCCAGCT 194

QY 61 CGCCTCTCTCGCGGGACCCCGCGCTCCCGACCCCTCCCGGGTCCCGGGCCCGAGCCC 120
DB 195 CGCCTCTCTCGCGGGACCCCGCGCTCCCGACCCCTCCCGGGTCCCGGGCCCGAGCCC 254

QY 121 CCTCCGGGCGCTCCCGAGCCCTCCCTTCTTCCGGCGGCGCCCGCCCTCTCTCGGGGG 180
DB 255 CCTCCGGGCGCTCCCGAGCCCTCCCTTCTTCCGGCGGCGCCCGCCCTCTCTCGGGGG 314

QY 181 CGAGTTTCAGGACGCTGCGTCTGCTGCGACGCTGGGAAGCCCTGGCCCGGCAACC 240
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Qy 241 CCGC 244
Db 375 CCGC 378

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Job time : 314.31 secs